A Genome-Wide Association Study of Diabetic Kidney Disease in Subjects With Type 2 Diabetes

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Abstract

Identification of sequence variants robustly associated with predisposition to diabetic kidney disease (DKD) has the potential to provide insights into the pathophysiological mechanisms responsible. We conducted a genome-wide association study (GWAS) of DKD in type 2 diabetes (T2D) using eight complementary dichotomous and quantitative DKD phenotypes: the principal dichotomous analysis involved 5,717 T2D subjects, 3,345 with DKD. Promising association signals were evaluated in up to 26,827 subjects with T2D (12,710 with DKD). A combined (T1D+T2D) GWAS was performed using complementary data available for subjects with T1D, which, with replication samples, involved up to 40,340 diabetic subjects (and 18,582 DKD cases).

Analysis of specific DKD phenotypes identified a novel signal near *GABRR1* (rs9942471, $p=4.5\times10^{-8}$) associated with 'microalbuminuria' in European T2D cases. However, no replication of this signal was observed in Asian subjects with T2D, or in the equivalent T1D analysis. There was only limited support, in this substantially enlarged analysis, for association at previously-reported DKD signals, except for those at *UMOD* and *PRKAG2*, both associated with 'eGFR'.

We conclude that, despite challenges in addressing phenotypic heterogeneity, access to increased sample sizes will continue to provide more robust inference regarding risk-variant discovery for DKD.

Introduction

Progressive loss of renal function represents one of the most serious complications of diabetes, yet strategies for prevention and management are suboptimal. One of the principal obstacles to improved clinical interventions remains rudimentary understanding of the processes whereby sustained exposure to elevated levels of glucose (and/or other manifestations of the diabetic state) leads to progressive disturbance of renal morphology and function (1).

There is considerable variation in the progression and severity of renal complications of diabetes (collectively, diabetic kidney disease [DKD]). The prevalence of DKD in subjects with T2D is ~30-50%: some patients experience a relatively rapid decline in renal function, whilst others maintain normal renal function despite decades of suboptimal glycemic control (2). The factors influencing this variation in outcome have not been fully characterised, but substantial evidence supports a genetic contribution. As in type 1 diabetes (T1D), DKD in those with type 2 diabetes (T2D) aggregates in families (3, 4), and the prevalence of DKD in T2D differs considerably between ethnic groups (5-7).

These observations indicate that the identification of genetic variants influencing DKD predisposition should accelerate characterization of the biological basis of DKD. In contrast with most complex multifactorial traits, efforts to apply candidate gene and genome wide association studies (GWAS) approaches to DKD have met with limited success (8-11). Many genetic associations have been reported, but few robustly replicated loci have emerged. This likely reflects the comparatively small sample sizes of previous studies, such that power would have been limited to detection of common loci of unusually large effect. In the case of DKD in T2D, this is likely to have been compounded by the heterogeneity of the phenotype: autopsy studies indicate that only ~50% of chronic kidney disease (CKD) in T2D can be attributed to classical diabetic nephropathy (12). The success of equivalent GWAS efforts for CKD (for which several replicated loci have been described) provides reassurance that it is possible to identify variants with broad impact on the progression of renal disease, irrespective of the dominant pathology (13).

Reduced kidney function, reflected by the estimated glomerular filtration rate (eGFR) and end-stage renal disease (ESRD), and dysfunction of the glomerular filtration barrier, reflected by albuminuria, can develop independently. This suggests that the two cardinal features of DKD involve distinct disease mechanisms and may be subject to different genetic effects. Albuminuria is known to be a poor predictor of diabetes-related ESRD, especially in the early stages, and regression to normoalbuminuria is common in patients with microalbuminuria (14).

These observations provide confidence that the combination of increased sample size and improved definition of DKD phenotypes should enable risk-variant detection and uncover mechanisms that contribute to renal dysfunction in diabetes. In particular, the separation of cases into phenotypic classes based on disease stage and/or phenotype manifestations, incorporating information on both albumin excretion and eGFR, can be expected to increase etiological homogeneity and augment power for locus identification (14-16).

The SUMMIT (SUrrogate markers for Micro- and Macro-vascular hard endpoints for Innovative diabetes Tools) consortium adopted such a strategy to perform a GWAS for DKD in subjects with T1D (17). Here, we report on equivalent analyses conducted in the context of T2D, as well as those from a combined (T1D+T2D) analysis involving up to 40,340 subjects.

Methods

Diabetic kidney disease phenotype definitions

Not all patients with DKD will develop every form of the disease or progress to the most severe stage of ESRD. Dysfunction of the glomerular barrier, represented by albuminuria, and reduced kidney function, represented by eGFR, can develop independently. To explore the disease severity spectrum and the different disease processes represented by eGFR and albuminuria, we defined seven binary phenotypes using clinical measures of albumin creatinine ratio (ACR), AER and eGFR (Table 1 [T2D-only] and Supplementary Table 8 [T1D+T2D]). The phenotype definitions were aligned to other large-scale genetic studies of T1D-DKD in SUMMIT (17) and the Diabetic Nephropathy Collaborative Research Initiative (DNCRI) (18). The definition of chronic kidney disease was also aligned to that used by the CKDGen consortium (eGFR<60 mL/min/1.73m^2) although we restricted cases and controls to those with diabetes (13).

We used AER measured over-night (µg/min), during 24 hours (mg/24 h), or as a spot measurement of ACR (mg/mmol) or eGFR calculated using the Modification of Diet Renal Disease Study Group (MDRD) formula (eGFR=32788 x Serum Creatinine (µmol/L)$^{-1.154}$ x Age$^{-0.203}$ x [0.742 if female]) to classify disease stage and severity. We based the control definition on either AER or ACR as most studies had measured either. In the studies that had measured both, 2/3 measures for AER and ACR had to meet the control criteria (Table 1). We were unable to exclude albuminuric patients that presented as normoalbuminuric due to prescribed renin-angiotensin system blockers. Since reduced kidney function (reflected by eGFR) and dysfunction of the glomerular filtration barrier (reflected by albuminuria) can develop independently, we did not exclude individuals with albuminuria from the controls for the eGFR-defined phenotypes and vice versa. In subjects with T2D, ~46% of normoalbuminuric controls had an eGFR<60 mL/min/1.73m^2 (1,098/2,372).

In all, we defined seven dichotomous phenotypes:

- the 'all DKD' phenotype, our primary phenotype, designed to capture the broadest set of DKD phenotypes;
- the 'microalbuminuria' phenotype (equivalent to 'early DKD' from Sandholm et al, 2017) (17) to identify variants that contribute to early dysfunction of the glomerular barrier;
- the 'late DKD' phenotype to identify variants that contribute to severe glomerular barrier dysfunction;
- two 'ESRD' related phenotypes focused on identification of variants associated with end stage renal failure, comparing those with ESRD either to control subjects without any DKD ('ESRD vs controls') and relative to control subjects without ESRD ('ESRD vs no ESRD');
- the chronic kidney disease ('CKD') phenotype to identify variants that contribute to reduced kidney function (eGFR);
- the 'CKD and DKD' phenotype to identify any variants that may contribute to the development of kidney disease irrespective of glomerular barrier dysfunction or reduced kidney function; and
- estimated glomerular filtration rate ('eGFR'), a continuous phenotype, to identify variants that play a role in kidney function that may not be detected by the analysis of the binary DKD phenotypes. The eGFR measures were not transformed as they

approximated a normal distribution (Supplementary Figure 1).

Study populations

We identified DKD cases and controls in subjects with T2D from the Scania diabetes registry (SDR) (19), the Genetics of Diabetes and Audit Research in Tayside Scotland (GoDARTS) study (20), the Steno Diabetes Centre (21) and the BENEDICT (Bergamo Nephrologic Diabetes Complications Trial, Italy) A and B studies (22). We identified independent replication studies in populations of European descent (deCODE, the Family investigation of nephropathy and diabetes [FIND] study, the DIabetes REgister in VAsa region [DIREVA] study, the Diagnostic Optimization and treatment of diabetes and its complications in the Chernihiv region [DOLCE] study, the Malmo Diet and Cancer Study [MDC], Inter99, Vejle Diabetes Biobank and the Anglo-Danish-Dutch study of Intensive Treatment In PeOple with screeN detected diabetes in primary care [ADDITION]), and Asian descent (RIKEN, the Singapore Diabetic Cohort Study [SDCS], the Hong Kong Diabetes Registry [HKDR] and the Singapore Study of Macro-angiopathy and Micro-vascular Reactivity in Type 2 Diabetes [SMART2D] study) (Supplementary Table 1).

We combined the subjects with T2D with non-overlapping samples from the study of DKD in subjects with T1D (17). Replication studies (of DKD in subjects with T1D) (17), were also used for replication in the combined analysis of T1D+T2D (Supplementary Table 1). None of these studies overlapped with samples included in the analysis of eGFR and CKD by the CKDGen consortium (13).

Genome-wide genotyping and imputation

The T2D discovery cohorts were genotyped on the Affymetrix SNP 6.0, the Illumina Omni express array and the Illumina 610Quad arrays (Supplementary Table 4). Individual study centres excluded SNPs for minor allele frequency (MAF) <1%. SNPs with a MAF 1-5% were excluded if the Hardy-Weinberg equilibrium (HWE) test $p<1\times10^{-4}$ or the call rate <99%. SNPs with MAF ≥5% were excluded if the HWE $p<5.7\times10^{-7}$ or the call rate <95% (23). Samples were excluded if: their call rate was <95%; genotype heterozygosity was >3SD from the study sample mean; or they failed gender checks. Based on principal component analysis: population outliers were removed if they were not of European descent (compared to the 1000G populations) or fell >3SD away from the population means of the first two principal components for samples of European descent. Duplicates were removed but related individuals were retained for genotype imputation.

Genotypes were prephased using SHAPE-IT (v2) (24) and imputed using IMPUTEv2 (25) against the March 2013 1000G version 1 reference panel using standard protocols and recommended settings.

Replication genotyping

Direct typing of twelve SNPs (rs11622435, rs12917707, rs17421627, rs1989248, rs2194025, rs2206136, rs4977388, rs61277444, rs6865390, rs7222331, rs9939609 and rs9942471) was performed in DIREVA samples using TaqMan allelic discrimination assays according to the manufacturer's protocol (Applied Biosystems, Carlsbad, CA). Sequenom multiplex genotyping was performed for the same SNPs in DOLCE using the standard protocol (26).

Statistical analysis

Heritability of diabetic kidney disease phenotypes

Narrow sense heritability was estimated by GCTA (v1.26) (27) from 4.5 million directly typed and imputed markers (info>0.75) in GoDARTS (Supplementary Table 1) for 'all DKD', 'CKD' and 'eGFR'. The sample size for these phenotypes exceeded the recommended threshold for reliable heritability estimates (N=3,160 based on a standard error ≤ 0.1) (28).

Genome-wide association analysis

Genome-wide association analyses were performed by individual study centres using an additive model whilst correcting for age, gender and duration of diabetes. We estimated allelic effects using the score test from SNPTESTv2 in unrelated samples for dichotomous traits (29). Association *p* values were calculated using EMMAX from a larger sample of related individuals whilst correcting for a kinship matrix (30). For 'eGFR' we estimated allelic effects and association *p* values using EMMAX (30).

Power calculations

We performed power calculations for dichotomous traits based on a MAF of 8%, an allelic OR range 1.05-2.00, and $\alpha=5\times10^{-8}$ (genome-wide significance). The power calculations were performed, for the discovery meta-analysis of 'all DKD', separately for the T2D-only (3,345 DKD cases and 2,372 DKD controls) and the combined (T1D+T2D; 5,908 DKD cases and 4,965 DKD controls) meta-analyses

At $\alpha\leq5\times10^{-8}$, we had >80% power to detect an allelic OR>1.40 in the T2D-only discovery analysis (Supplementary Figure 2C) and an allelic OR>1.25 (Supplementary Figure 2B) in the combined discovery analysis. We also performed power calculations for the reported DKD loci, as above, but using $\alpha=9\times10^{-4}$ (this α accounts for the number of loci tested but not the number of phenotypes analysed). In the combined analysis (T1D+T2D, 'all DKD') we had >80% power to detect variants with an allelic OR>1.20 (Supplementary Figure 2A).

Discovery meta-analysis

Two discovery meta-analyses were performed: one that included summary statistics estimated from subjects with T2D-only and a second that combined T2D-only analyses with equivalent analyses in subjects with T1D (17). Individual study summary statistics were centrally filtered for a minor allele count in either cases or controls <10 and an info score <0.4 for imputed variants.

EMMAX *p* values were combined in a sample size weighted z-statistic meta-analysis using METAL (version 25/03/2011) (31). Effect estimates were combined in a fixed-effect-inverse-variance weighted meta-analysis using GWAMA (v2.1) (32). Meta-analysis results were restricted to allelic effects estimated in ≥ two studies. For binary traits, independent variants (>100Kb apart) were selected for replication from the T2D-only analysis based on association $p \leq 5\times10^{-6}$ and from the combined (T1D+T2D) analysis based on $p \leq 1\times10^{-6}$. For 'eGFR', SNPs were chosen for replication based on association $p \leq 5\times10^{-6}$ in subjects with T2D or $p<1\times10^{-6}$ in the combined analysis. SNPs associated with 'eGFR' at $p \leq 5\times10^{-4}$ in either 'eGFR' analysis (T2D only or T1D+T2D) which had also been reported at $p \leq 5\times10^{-8}$ with eGFR by the CKDGen consortium were also included in the list of SNPs for replication (13).

Replication

We sought replication for 164 lead variants in thirteen studies of T2D-DKD for which it was possible to obtain *in silico* replication from available GWAS data or replication from where *de novo* genotyping (DIREVA and DOLCE) (Figure 1). Replication studies aligned their DKD phenotypes with those employed in the SUMMIT GWAS. Although association results for the lead variants were recovered for all compatible DKD phenotypes available in the replication samples (Supplementary Table 1), joint meta-analysis results were reported for those phenotypes where the primary GWAS associations exceeded the thresholds above.

As with the discovery, meta-analysis effect estimates from replication studies were combined using GWAMA (v2.1) (32), and EMMAX *p* values using METAL (version 25/03/2011) (31).

Known DKD variants

We examined the literature for variants that have been associated with DKD from candidate gene ($p<0.05$) and GWA ($p\leq5\times10^{-8}$) studies. Sixty-one variants were identified and aligned to the reported risk allele for binary traits (or the trait-raising allele for quantitative traits). We assessed both direction of effect and strength of association in the present study for those phenotypes that most closely matched the original report (but irrespective of type of diabetes).

Genetic risk score analysis

We included variants ($p\leq5\times10^{-8}$) from GWAS to generate genetic risk scores (GRS) for: coronary artery disease (CAD) (33); body mass index (BMI) (34); waist-hip-ratio adjusted for BMI (WHR) (35); low-density lipoprotein cholesterol (LDL-C); triglycerides (TRIG); high-density lipoprotein cholesterol (HDL-C) (36); fasting insulin (FI); insulin resistance (IR) (37-39); fasting glucose (FG) (38); T1D (40); T2D (41); and systolic blood pressure (SBP) (42). The relationship between the GRS and the DKD phenotype was calculated using an inverse-variance weighted method described in Ehret et al., 2011(42).

Results

DKD definitions: We considered seven dichotomous phenotypes designed to capture the spectrum of DKD (see **Methods**), and 'eGFR'. We aimed to identify variants that influence multiple stages in DKD progression, as well as those that have more stage-specific effects. The principal definition ('all DKD') included 3,345 T2D subjects with any form of DKD (ranging from microalbuminuria through to ESRD) as cases, and 2,372 T2D subjects, normoalbuminuric despite >10 years duration of diabetes, as controls. The other six dichotomous phenotypic comparisons are described in Table 1 (see also **Methods**).

Contribution of Genetic Variants to DKD: The genetic variation, explained by the SNPs on the genotyping array and estimated using GCTA (v1.26) (30) in up to 6,335 subjects with T2D from the GoDARTS, was highest in 'CKD' (h^2=0.12) and similar for 'all DKD' (h^2=0.08) and 'eGFR' (h^2=0.07) (Supplementary Table 2). We restricted analyses to phenotypes with sample sizes deemed sufficient for accurate estimation of heritability (N≥3,160 to obtain an SE≤0.1) (28).

GWAS for DKD in T2D: The DKD discovery analysis combined GWAS data from four studies of European descent: GoDARTS (20), SDR (19), STENO (Denmark) (21) and the BENEDICT study (phases A and B, Italy) (22) (Table 1, Supplementary Table 3). For the principal ('all DKD') analysis, the sample size of the discovery T2D-only meta-analysis had >80% power to detect variants with MAF≥8% and allelic OR>1.40 (Supplementary Figure 2C). The number of variants meta-analysed for each DKD phenotype varied between 5,864,445 in the 'ESRD vs no ESRD' phenotype and 9,263,264 in the 'all DKD' phenotype (Supplementary Table 4). These differences reflect the minor allele count exclusion filter.

Manhattan and QQ plots of discovery *p*-values for each of the eight DKD phenotypes were well calibrated, and several showed a modest excess of significant associations (Supplementary Figure 3). In the discovery GWAS, only one locus reached genome-wide significance: *PLCB4 (*encoding 1-Phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta-4) on chromosome 20. The lead variant rs2206136 was associated with the 'CKD' phenotype (EAF 42%; OR 1.20 [1.08, 1.34]; $p=2.1\times10^{-8}$) (Table 2; Supplementary Figure 3A).

To extend power to detect associations of lesser effect, and to replicate the *PLCB4* association, we identified 139 loci with SNP associations exceeding $p\leq5\times10^{-6}$ in at least one of the seven dichotomous DKD analyses. We also identified 22 loci (25 lead variants) for replication from the 'eGFR' analysis (based on either $p<5\times10^{-6}$ in our 'eGFR' analyses alone, or $p<5\times10^{-4}$ in our analysis and a genome-wide association [$p<5\times10^{-8}$] reported by the CKDGen consortium) (Supplementary Figure 3Q) (13). We sought replication for 164 lead variants in thirteen studies of T2D-DKD (nine involving European subjects, and four involving Asian subjects) for which it was possible to obtain association analyses based on either *in silico* (from existing GWAS) or *de novo* genotyping (Figure 1). Replication studies recoded their DKD phenotypes to align definitions with those employed in the SUMMIT GWAS. Although association results for the lead variants were recovered for all compatible DKD phenotypes available in the replication samples (Supplementary Table 1), joint meta-analysis results are reported for only those phenotypes where the primary GWAS associations exceeded the thresholds above (Supplementary Table 5). The replication samples available for the 'all DKD' phenotype included up to 3,999 T2D subjects of European ancestry (1,270 cases) and 17,111 (8,095 cases) from Asia (Supplementary Table 1).

The ‘CKD’ association near *PLCB4* did not replicate in either European or Asian data (joint analysis ; $OR_{Asian+Euro}$ 1.12 [1.05, 1.19]; p=2.1×10^{-4}) (Table 2). Joint analysis of dichotomous DKD phenotypes identified one novel SNP association that marginally exceeded genome-wide significance (p=5×10^{-8}, without adjustment for the multiple GWAS we performed) (Table 2). This signal, on chromosome 6, is centred on rs9942471 and lies ~7kb upstream of *GABRR1* (encoding the rho1 subunit of the GABA type a receptor). The major allele was associated with increased risk of ‘microalbuminuria’ in subjects of European ancestry (Joint analysis; EAF 64%; OR_{Euro} 1.25 [1.16, 1.34]; p=4.5×10^{-8}) (Figure 2, Table 2). Associations of rs9942471 with other DKD phenotypes are given in Supplementary Table 6.

Rs9942471 is in high LD (r^2>0.8) with the lead eQTL variant for *GABRR1* expression in artery, oesophagus and skin (p≤4×10^{-8}) and the major allele is associated with decreased expression (42). However, there was no evidence for replication of this SNP in T2D subjects of Asian ancestry only (EAF 90%; OR_{Asian} 0.99 [0.87, 1.13]; p=0.91) although the higher frequency of the effect allele in Asians (90%) compared to Europeans (64%) reduces the power to detect an effect in subjects of Asian descent. Ethnic differences in regional LD could have contributed to failed replication: rs9942471 may be a better marker of the shared causal variant in subjects of European descent. However, this seems unlikely given broad similarity of LD patterns across subjects of European and Asian descent (estimated separately from the 1000G population).

Replication samples for the ‘eGFR’ phenotype included 8,749 subjects of European and 9,071 subjects of Asian ancestry with T2D (Figure 1). Joint analysis of discovery and replication results captured the well-established association with variants near *UMOD* (uromodulin), centred on rs11864909 ($\beta_{Asian+Euro}$ 2.34 [1.68, 3.00] mL/min/1.73m^2; p=4.4×10^{-}

[12]) (Table 2). There was no difference in effect by diabetes type: the effect estimate in subjects with T1D (β_{T1D} 1.23 (-0.05, 2.51), p=0.06) overlapped the effect size in subjects with T2D (17). We also compared the effects of variants associated with DKD phenotypes in subjects with T2D from Table 1 with their effects in equivalent DKD phenotypes in subjects with T1D (17) (Supplementary Table 7).

Combined T1D and T2D analysis: To increase power to detect loci that contribute to processes involved in the development of DKD irrespective of diabetes subtype, we combined the results from the primary GWAS meta-analysis for T2D-DKD phenotypes with those for the corresponding T1D-DKD phenotypes (Supplementary Table 4, 9) (17). The combined discovery meta-analysis of 'all-DKD' included 10,873 diabetic subjects of European descent (5,908 cases) and provided >80% power ($\alpha=5\times10^{-8}$) to detect a SNP association with an allelic OR>1.25 for variants with MAF >8% (Supplementary Figure 2B). The number of variants meta-analysed ranged from 7,959,015 for 'ESRD vs no ESRD' to 9,364,702 for the 'all DKD' phenotype (Supplementary Table 4).

No significant associations were detected for dichotomous DKD phenotypes in the combined (T1D+T2D) meta-analysis (Supplementary Figure 4; Supplementary Table 9). The combined meta-analysis for 'eGFR' highlighted a novel genome-wide significant association involving a cluster of variants on chromosome 2 led by rs1974990 (EAF 8%; β 4.07 [2.61, 5.52] mL/min/1.73m^2; $p=4.8\times10^{-8}$) and mapping near *SSB* (encoding Sjogren syndrome antigen B) (Table 2).

As in the T2D-only analysis, we selected 47 loci for replication (30 with $p<1\times10^{-6}$ with at least one of the DKD phenotypes) from the combined (T1D+T2D) GWAS, and an additional 17 loci from the equivalent analysis of 'eGFR'. The combined association *p*-value for rs9942471 ('microalbuminuria'; OR 1.10 [1.02, 1.19]; p=0.001) did not reach the threshold for replication. Lead variants at these 47 loci were tested for all DKD phenotypes available in the relevant replication samples in subjects with T1D or T2D (Supplementary Table 1): meta-analysis results were only reported for those phenotypes that contributed to discovery-stage associations. This joint, combined (T1D+T2D) analysis generated a substantially enlarged data set for the 'all-DKD' phenotype (40,640 subjects [18,582 cases]) (Figure 1). However, none of the variants selected for replication from the dichotomous phenotypes reached genome-wide significance ($p \leq 5\times10^{-8}$).

The joint, combined analysis for 'eGFR' in subjects European and Asian descent included 31,562 subjects, and replicated known associations near *UMOD* (rs11864909; $\beta_{\mathrm{Asian+Euro}}$ 2.11 [1.52, 2.70]; $p=2.3\times10^{-12}$) and *PRKAG2* (rs10224002 $\beta_{Asian+Euro}$ 2.01 [1.30, 2.72], $p=2.7\times10^{-8}$) (Table 2; Supplementary Figures 5 and 6). The *PRKAG2* was non-significant ($p \leq 5\times10^{-8}$) in individual analyses of 'eGFR' in T2D-only (β_{Euro} 2.13 [1.28, 2.98]; $p=8.5\times10^{-7}$) or T1D-only (β_{Euro} 1.23 [-0.19, 2.65]; p=0.09) and effect sizes did not differ by type of diabetes.

The association at *SSB*, detected in the combined 'eGFR' analysis, did not replicate (rs1974990, β 0.04[-2.69, 2.76] mL/min/1.73m^2; p=0.98) and, in the joint, combined analysis was no longer genome-wide significant ($\beta_{Asian+Euro}$ 3.17 [1.88, 4.45] mL/min/1.73m^2; $p=1.4\times10^{-6}$) (Table 2).

Evaluating previous association claims: Of the 61 published loci, for which there are published claims of association with T1D-DKD or T2D-DKD (8), 55 of these associations were represented by variants contributing to our meta-analyses of DKD phenotypes in either subjects with T2D-only or T1D+T2D. Two of these, the 'eGFR' associations at *UMOD* and *PRKAG2,* replicate at genome-wide significance in our data (Table 2). We tested the association of the remaining 53 lead variants in the T2D-only and combined analyses (Supplementary Figure 6). Fourteen variants were associated with a DKD phenotype corresponding to the original report at nominal significance ($p<0.05$) but only 10 of these were directionally consistent with previous reports (Supplementary Table 10). At a more stringent significance level ($p<9\times10^{-4}$) that accounts for the 55 variants tested (but not the multiple phenotypic categories), only two variants were associated with a DKD phenotype that corresponded to the original report, both of them in the combined (T1D+T2D) analysis, and both directionally consistent with previous reports. These two SNPs were rs2838302, near *SIK1,* associated with 'ESRD vs no ESRD' (EAF 8%; OR 1.39 [1.12, 1.74]; $p=3.9\times10^{-4}$) and rs7583877, near *AFF3*, associated with 'ESRD versus no ESRD' (OR 1.22 [1.13, 1.32]; $p=4.8\times10^{-4}$) (Supplementary Table 10). When we took account of the substantial participant overlap between the original reports and the samples in the present study, apparent replications failed to reach nominal ($p<0.05$) significance (though, for these, the sample sizes available for independent replication were often small). Thus, other than the 'eGFR' associations at *UMOD* and *PRKAG2,* we found limited evidence in this study to corroborate previously-reported DKD associations, despite, for most variants, sample sizes considerably larger than those included in the original report. Validation of previously-reported DKD associations could be complicated by differences in phenotype definitions and/or analytical methods between this study and published reports. We could not assess whether the *UMOD* or *PRKAG2* allelic effects were different in this study compared to those reported by CKDGen consortium as the allelic effects were not on the same scale (e.g. untransformed vs log transformed).

Genetic overlap with risk factors: Several exposures and diseases have been reported to increase DKD risk in epidemiological studies (1, 2, 43). To explore the extent to which these reflect shared genetic background, we constructed weighted genetic risk scores (GRS) for twenty traits related to diabetes (37, 39-41), insulin resistance (38), obesity (34, 35), hypertension (42), coronary artery disease (33), and lipids (36). These GRS, constructed from signals identified ($p<5\times10^{-8}$) in previously-published GWAS, included between 10 and 96 SNPs per phenotype. We tested the association of these GRS with each of the DKD phenotypes from this study, in both T2D-only and combined (T1D+T2D) data sets (42).

After Bonferroni correction ($p\leq2.5\times10^{-3}$, which accounts for the number of trait GRS but not the number of DKD phenotypes): In subjects with T2D a GRS for increased waist-to-hip ratio (WHR) ($p=4.8\times10^{-4}$) was associated with increased risk of 'ESRD vs no ESRD'; and a GRS for increased BMI was associated with 'all DKD' ($p=1.8\times10^{-4}$) and 'late DKD' ($p=1.8\times10^{-3}$) phenotypes. A similar pattern of association for the BMI GRS was observed in the combined (T1D+T2D) 'all DKD' analysis ($p=2.4\times10^{-5}$) (Supplementary Table 11 and Figure 3). This last result survives additional correction ($\alpha=1.6\times10^{-4}$) for the 16 DKD phenotypic comparisons considered.

There is evidence implicating insulin resistance in the pathogenesis of DKD, and we wanted to understand whether the BMI GRS associations might reflect obesity-related insulin resistance (44, 45). We focused on the effects two alternative GRS for insulin resistance on DKD. The first, comprising lead variants (N=10) associated with increased fasting insulin (BMI-adjusted) (37), was associated with increased risk of ESRD in subjects with T2D ('ESRD vs no ESRD' $p=1.6\times10^{-3}$; 'ESRD vs controls' $p=1.7\times10^{-3}$) (Supplementary Table 11 and Figure 3). The second, comprising lead variants from 53 loci associated with high fasting insulin

(BMI-adjusted), low HDL-C and high triglycerides (39), failed to show any association with DKD phenotypes. These findings provide some support for the causal contribution of insulin resistance and obesity to DKD pathogenesis. However, there is potential that some of these effects reflect collider bias (46) and additional larger studies will be required to substantiate this inference.

Discussion

This study represents the largest study of the genetic basis of DKD in subjects with T2D to date, extending previous reports with respect to sample size and range of DKD phenotypes. We aimed to overcome some of the limitations of earlier studies in this area, and to develop insights into the pathogenesis of DKD. Despite sample sizes that exceeded 40,000, the yield of novel discoveries was modest. There were no significant ($p<5x10^{-8}$) genetic associations with 'all DKD' that was best-powered definition on sample size. The relatively large sample size came with increased phenotypic (and likely genetic) heterogeneity: it was for this reason that we examined a range of DKD phenotypes that might offer better power to detect genetic associations with more restricted phenotypic impacts.

This approach successfully identified a novel locus, *GABRR1* (led by rs9942471), for 'microalbuminuria' in European subjects with T2D. The variants, near *GABRR1*, reached a level of significance (p<$5x10^{-8}$) that has typically been associated with robust, reproducible association in common disease GWAS. *GABRR1* expression is upregulated in renal biopsies form DKD subjects (compared to controls) and in other non-diabetic kidney diseases characterised by glomerular scarring and inflammation (47). The variants were associated with *GABRR1* expression in aorta, oesophageal mucosa and skin in GTEx. However, we found no replication of the *GABRR1* association in subjects of European ancestry with T1D-DKD, nor amongst subjects of Asian ancestry with T2D, though differences in risk-allele frequencies between these two ancestries and the modest size of the replication datasets at this locus reduce the power of the latter analysis. Our overall assessment is that this association should be considered provisional until it is possible to undertake further rounds of adequately-powered replication that could establish the definitive status of this variant and this locus should also be assessed for effects on DKD progression in longitudinal studies.

Even in the absence of specific signals of association with DKD, it is possible to use the aggregate pattern of association across the genome to identify more subtle genetic effects. The GRS analyses described here provide genetic support for the causal contribution of obesity to the development of T2D-DKD. This echoes strong epidemiological data, and mirrors equivalent analyses in T1D-DKD (48, 49). However, we cannot exclude that these associations may partly reflect collider bias (46): subjects with high BMI are likely to have a longer duration of diabetes and thus a higher chance of developing complications. Analyses using genetic instruments (GRS) for variation in insulin sensitivity produced variable results with respect to T2D-DKD, but indicate that the BMI effects may be partially mediated via obesity-related insulin resistance (37). There is substantial epidemiological data to support this link between insulin resistance and DKD risk (44, 45).

The modest yield of association signals, and the limited replication of previous claims of DKD association, emphasises challenges associated with the identification of DKD-risk variants. For many complex traits, these have been overcome through a combination of increased sample size and phenotypic precision. Published genetic association studies of DKD have often used different definitions of DKD, which makes replication of previous findings difficult. In this study, we used phenotype definitions aligned to those used in the study of DKD in subjects with T1D (17). Standardising the phenotype definitions in this way allowed for seamless combination of the GWAS data across the two studies and may streamline subsequent efforts to study the genetics of DKD. The phenotype definitions applied to this study address some of the challenges associated with increasing sample size while maintaining phenotype precision, and should, in due course, support the identification of robust associations with DKD. It is clear that these phenotype definitions are not without limitations, in the absence of strong genetic signals we have few clues to which particular diagnostic configurations will be most productive for genetic discovery. Targeting the phenotypes that show the greatest heritability may provide a guide (14).

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Author Contributions

Central data analysis was performed by: N.R.v.Z., E.A., N.S., N.W.R., D.Z., E.F., S.C. and M.I.M. Data generation was performed by N.R.v.Z., E.A., H.D., C.L., F.S.c., M.K., J.L., G.J., A.O.Y.L., H.M.L., C.K.P.L., J.C.N.C., H.K.D.R.T.P.G., S.F.A., R.D., T.S.H.C., A.-J.M., T.W.3.G.S.G., G.C., S.H., D.g., T.S.A., M.O.-M., A.L., C.C., N.G., I.B., O.M., S.C.L., R.C.W.M., V.L., S.S.R., J.C.F., O.P., T.H., S.C., C.N.A.P., P.-H.G., L.C.G. and M.I.M. Individual study design was performed by E.A., N.S., H.D., P.M.M., C.F., N.P., R.M.v.D., G.J., J.C.N.C., M.M., M.O.-M., A.L., C.C., D.R.W., I.B., S.C.L., R.C.W.M., E.S.T., S.M., T.T., O.P., T.H., G.R., S.C., M.J.B., C.N.A.P., P.-H.G., H.M.C. and L.C.G. Local data analysis was peformed by N.R.v.Z., E.A., N.S., H.D., N.W.R., C.L., N.R.R., P.M.M., E.V., A.P., R.P.I.Jr, N.P., M.I., A.T., X.S., J.L., G.J., J.C.N.C., H.K.D.R.T.P.G., S.F.A., R.D., L.W., A.-J.M., S.D., M.G.P., G.C., M.M., S.H., L.T.H., T.S.A., P.A., C.-A.S., O.M., A.D.P., D.T., A.P.M., S.C.L., R.C.W.M., V.L., S.S.R., J.C.F., G.R., S.C., C.N.A.P. and H.M.C. The paper was prepared by N.R.v.Z., E.A., N.S., M.A., N.R.R., M.L., J.C.N.C., L.T.H., A.D.P., S.C.L., R.C.W.M., J.C.F., P.R., S.C., H.M.C., L.C.G. and M.I.M. Sample collection was conducted by C.F., V.H., F.S.c., E.R., M.L.M., N.P., M.L., R.M.v.D., A.O.Y.L., C.K.P.L., C.C.S., W.Y.S., J.C.N.C., H.K.D.R.T.P.G., S.F.A., T.S.H.C., A.-J.M., T.W.3.G.S.G., G.C., M.M., S.H., D.g., M.O.-M., A.L., C.C., D.R.W., I.B., O.M., A.P.M., S.C.L., R.C.W.M., E.S.T., V.L., T.T., A.S.K., S.S.R., J.C.F., D.D., O.P., T.H., P.R., G.R., S.C., C.N.A.P., P.-H.G., H.M.C., L.C.G., A.K., G.J., A.P.M., R.C.W.M., E.S.T. and L.C.G. N.R.v.Z and M.I.M are the guarantors of this work and, as such, had full access to all the data in the study and take responsibility for the integrity of the data and the accuracy of the data analysis.

Duality of Intereast

P. R. has given lectures for Astra Zeneca, BMS and Boehringer Ingelheim, has served as a consultant for AbbVie, Astra Zeneca, BMS, Eli Lilly, Boehringer Ingelheim, Astellas, Janssen, and Novo Nordisk; all fees were given to the Steno Diabetes Center that has equity interest in Novo Nordisk. E.F. is an employee of and owns stock in Pfizer, Inc. W.Y.S. is co-founder of GemVCare, established under the Technology Start-up Support Scheme for Universities (TSSSU) from the Hong Kong Government Innovation and Technology Commission. J.C.N.C. is co-founder of GemVCare, established under the Technology Start-up Support Scheme for Universities (TSSSU) from the Hong Kong Government Innovation and Technology Commission. R.C.W.M. is co-founder of GemVCare, established under the Technology Start-up Support Scheme for Universities (TSSSU) from the Hong Kong Government Innovation and Technology Commission. J.C.F. has received a consulting honorarium from Merck. P.-H.G. has received lecture honoraria from AstraZeneca, Boehringer Ingelheim, Eli Lilly, Genzyme, MSD, Novartis, Novo Nordisk, and Sanofi, and research grants from Eli Lilly and Roche. P-HG is also an advisory board member for AbbVie, Boehringer Ingelheim, Eli Lilly, Janssen, Medscape, MSD, Novartis and Sanofi. M.I.M. serves on advisory panels for Pfizer and Novo Nordisk; has received honoraria from Lilly, Pfizer, and Novo Nordisk; and M.I.M has received research support from Lilly, Pfizer, Novo Nordisk, Servier, Takeda, Roche, Merck, Janssen, Abbvie, Boehringer Ingelheim, Astra Zeneca and Sanofi Aventis.

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Table 1: Genome-wide association study characteristics by diabetic kidney disease phenotypes in subjects with type 2 and type 1 diabetes

Analysis	Case definition	Control definition	Subjects with type 2 diabetes		Subjects with type 1 diabetes	
			#Cases	#Controls	#Cases	#Controls
All Diabetic kidney disease (DKD)	**All DKD**: Microalbuminuria OR Late DKD OR end-stage renal disease (ESRD)	Normoalbuminuria (Albumin excretion rate [AER] <20 µg/min OR AER <30 mg/24 h OR ACR <2.5/3.5 mg/mmol for men/women) AND duration of T2D >10 years‡	3,345	2,372	2,563	2,593
Microalbuminuria*	**Microalbuminuria**: At least 2 out of 3 consecutive measurements with albumin excretion rate (AER) ≥20 AND <200 µg/min OR AER ≥30 AND <300 mg/24 hr OR albumin to creatinine ratio (ACR) ≥2.5/3.5 AND <25/35 mg/mmol for men/women;	Normoalbuminuria AND duration of T2D >10 years‡	1,989	2,238†	806	2,593
Late DKD	**Late DKD**: At least one measurement with AER ≥200 µg/min OR AER ≥300 mg/24 h OR ACR ≥25/35 mg/mmol for men/women) or end-stage renal disease (ESRD, estimated glomerular filtration rate (eGFR) < 15 mL/min/1.73m^2 OR kidney transplantation OR dialysis)	Normoalbuminuria AND duration of T2D >10 years‡	1,339	2,372	1,757	2,593
ESRD vs. controls	**ESRD**: eGFR<15 mL/min/1.73m^2 or renal dialysis or kidney transplant	No DKD AND duration of T2D >10 years‡	371	2,076	813	2,398
ESRD vs. no ESRD	ESRD (see above)	No ESRD AND duration of T2D >10 years‡	371	4,471	813	3,995
Chronic Kidney Disease (CKD)	**CKD**: eGFR < 60 mL/min/1.73m^2	No CKD AND duration of T2D >10 years‡	3,094	2,906	2,460	774
CKD and DKD	**CKD and DKD**: eGFR < 45 mL/min/1.73m^2 AND all DKD	No CKD AND no ESRD AND normoalbuminuria AND duration of T2D >10 years‡	897	1,610	1,750	1,385
eGFR	32788 x Serum Creatinine(µmol/L)$^{-1.154}$ x Age$^{-0.203}$ x [0.742 if female] (mL/min/1.73m^2)		9,197		3,961	

*Equivalent to the 'early DKD' phenotype from Sandholm et al., 2017 (17); †Not all studies were able to define microalbuminuria (due to limited information on microalbuminuric status) thus the case and control number is smaller than 'all DKD' and 'late DKD'; ‡The duration of diabetes for subjects with T1D was >15 years

Table 2: Five loci were associated ($p \leq 5 \times 10^{-8}$) with chronic kidney disease ('CKD'), 'microalbuminuria' and estimated glomerular filtration rate ('eGFR') in subjects with type 2 diabetes (T2D) or the combined analysis of T2D and type 1 diabetes (T1D+T2D)

			Discovery			Replication			Joint analysis		
CHR:BP	**Phenotype**	**SNP *Locus***	**EA/NEA (Info) EAF**	**OR/Beta (95%CI)**	**P**	**Ancestry**	**OR/Beta (95%CI)**	**P**	**OR/Beta (95%CI)**	**P**	**N**
20: 9351150	T2D 'CKD'	rs2206136 (*PLCB4*)	A/T (0.98) 0.42	1.20 (1.08-1.34)	2.1×10^{-8}	European	1.02 (0.91,1.15)	0.69	1.13 (1.05,1.21)	9.0×10^{-5}	11,900
						Asian and European	1.03 (0.94,1.13)	0.68	1.12 (1.05,1.19)	2.1×10^{-4}	13,813
6: 89948232	T2D 'microalbu-minuria'	rs9942471 (*GABRR1*)	A/C (0.99) 0.64	1.24 (1.15-1.34)	2.1×10^{-7}	European	1.32 (0.99,1.75)	0.06	1.25 (1.16,1.34)	4.5×10^{-8}	4,801
						Asian and European	1.11 (0.99,1.23)	0.12	1.15 (1.08,1.23)	1.2×10^{-5}	5,559
16: 20400839	T2D 'eGFR'	rs11864909 (*UMOD*)	T/C (1.00) 0.28	2.42 (1.28-3.56)	2.7×10^{-5}	European	2.22 (1.16,3.28)	4.1×10^{-5}	2.31 (1.54,3.09)	4.6×10^{-9}	12,343
						Asian and European	2.30 (1.48,3.12)	3.6×10^{-8}	2.34 (1.68,3.00)	4.4×10^{-12}	19,747
2: 170646916	T1D+T2D 'eGFR'	rs1974990* (*SSB*)	G/T (0.98) 0.08	4.07 (2.61,5.52)	4.8×10^{-8}	European	No replication available		4.07 (2.61,5.52)	4.8×10^{-8}	13,158
						Asian and European	0.04 (-2.69,2.76)	0.98	3.17 (1.88,4.45)	1.4×10^{-6}	14,828
7: 151415041	T1D+T2D 'eGFR'	rs10224002 (*PRKAG2*)	A/G (0.92) 0.74	1.75 (0.85-2.66)	1.5×10^{-4}	European	2.15 (0.93-3.37)	5.8×10^{-4}	1.89 (1.17,2.62)	3.4×10^{-7}	20,495
						Asian and European	2.42 (1.28,3.56)	3.2×10^{-5}	2.01 (1.30, 2.72)	2.7×10^{-8}	22,165
16: 20400839	T1D+T2D 'eGFR'	rs11864909 (*UMOD*)	T/C (0.99) 0.29	1.90 (1.05-2.74)	1.1×10^{-5}	European	2.22 (1.16,3.28)	4.1×10^{-5}	2.02 (1.36,2.69)	2.1×10^{-9}	16,304
						Asian and European	2.30 (1.48,3.12)	3.6×10^{-8}	2.11 (1.52,2.70)	2.3×10^{-12}	23,708

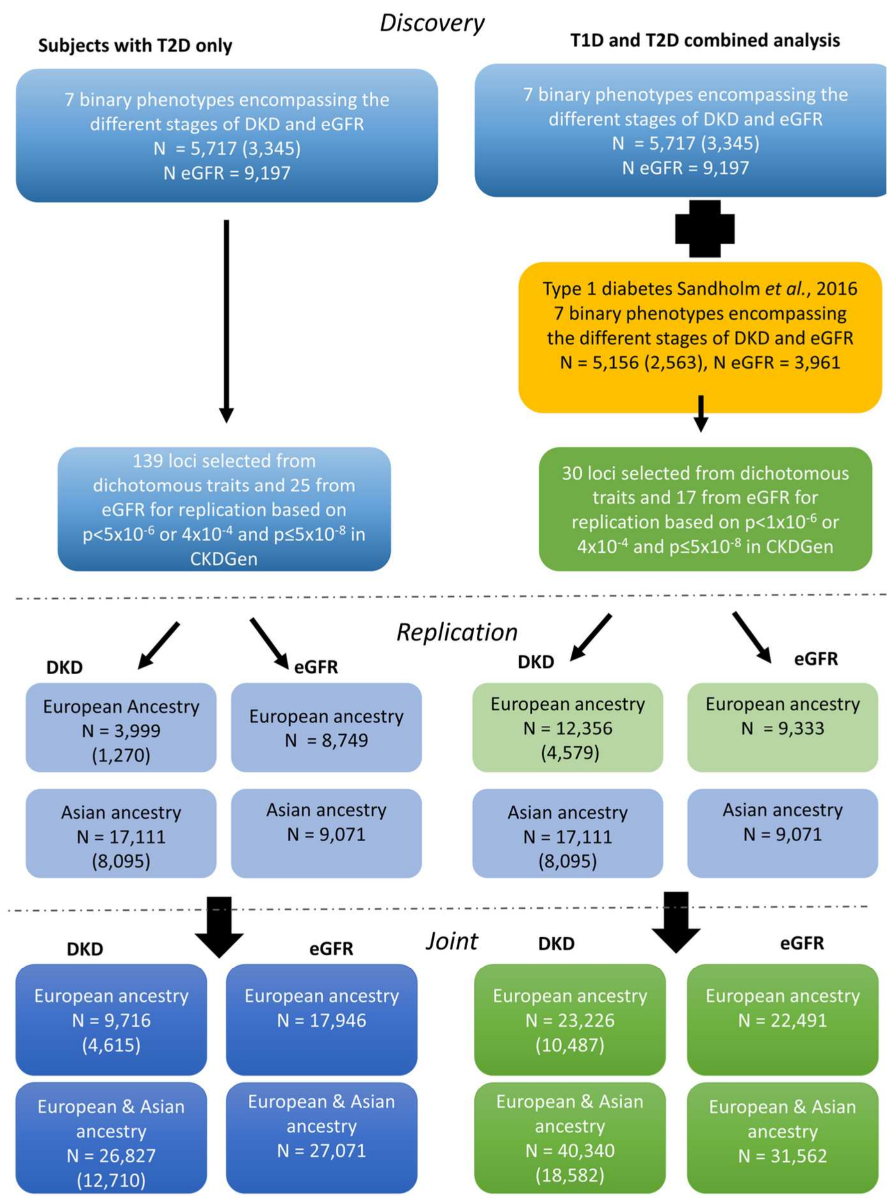
*rs1974490 was only available in the 1000G reference panel and was not imputed in the European studies used in the replications

Figures

Figure 1: Eight diabetic kidney disease (DKD) phenotypes were analysed in subjects with type 2 diabetes (T2D, blue boxes) and in a combined (green boxes) analysis of subjects with T2D or type 1 diabetes (T1D, yellow box). N indicates the total sample count for either the 'all DKD' (number of cases are given in brackets) or the 'eGFR' phenotypes and may vary by variant as well as by DKD phenotype. Replication was sought for 164 loci and 47 loci from each analysis respectively in subjects of European and Asian ancestry with either T1D or T2D.

Figure 2: A) Manhattan plot of p values from the meta-analysis of allelic effect on 'early diabetic kidney disease' in subjects with type 2 diabetes of European descent. The red line represents genome-wide significance (p<5x10^{-8}) and the blue line suggestive significance (p<1x10^{-6}). The peak represented by rs9942471 (p=4.5x10^{-8}), near *GABRR1* is highlighted in orange; **B)** A forest plot of allelic odds ratio (OR) and imputation information scores (RSQ) from individual studies (Study) that contributed to the discovery and replication (DIREVA) analyses of rs9942471 in 'microalbuminuria'; Rs9942471 genotypes were not available in Steno; and **C)** a Locuszoom plot of the signal near near *GABRR1* led by rs9942471 that was associated with early diabetic kidney disease in European subjects with T2D.

Figure 3: A heat map of genetic risk score associations with diabetic kidney disease (DKD) phenotypes in subjects with either type 1 diabetes or type 2 diabetes. A GRS for body mass index was significant after correction for multiple testing while other traits including systolic blood pressure were not associated with DKD phenotypes. Abbreviations used: chronic kidney disease ('CKD'), end stage renal disease ('ESRD') and estimated glomerular filtration rate ('eGFR').



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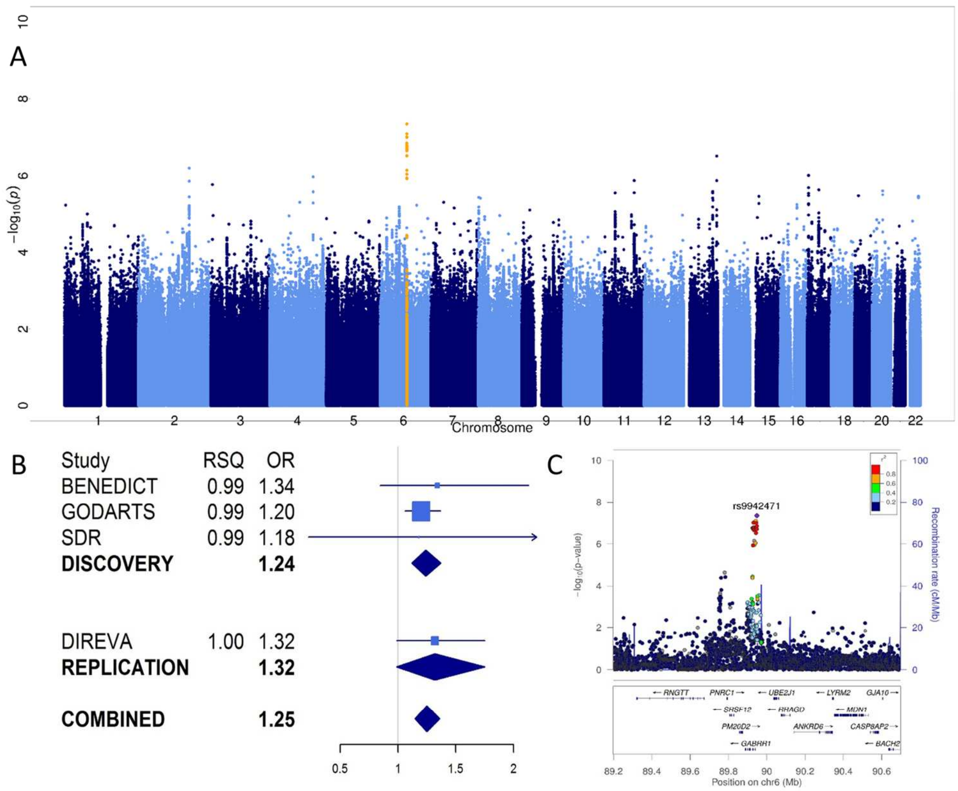

Figure 2: A) Manhattan plot of p values from the meta-analysis of allelic effect on 'early diabetic kidney disease' in subjects with type 2 diabetes of European descent. The red line represents genome-wide significance (p<5x10-8) and the blue line suggestive significance (p<1x10-6). The peak represented by rs9942471 (p=4.5x10-8), near GABRR1 is highlighted in orange; B) A forest plot of allelic odds ratio (OR) and imputation information scores (RSQ) from individual studies (Study) that contributed to the discovery and replication (DIREVA) analyses of rs9942471 in 'microalbuminuria'; Rs9942471 genotypes were not available in Steno; and C) a Locuszoom plot of the signal near near GABRR1 led by rs9942471 that was associated with early diabetic kidney disease in European subjects with T2D.

149x122mm (300 x 300 DPI)

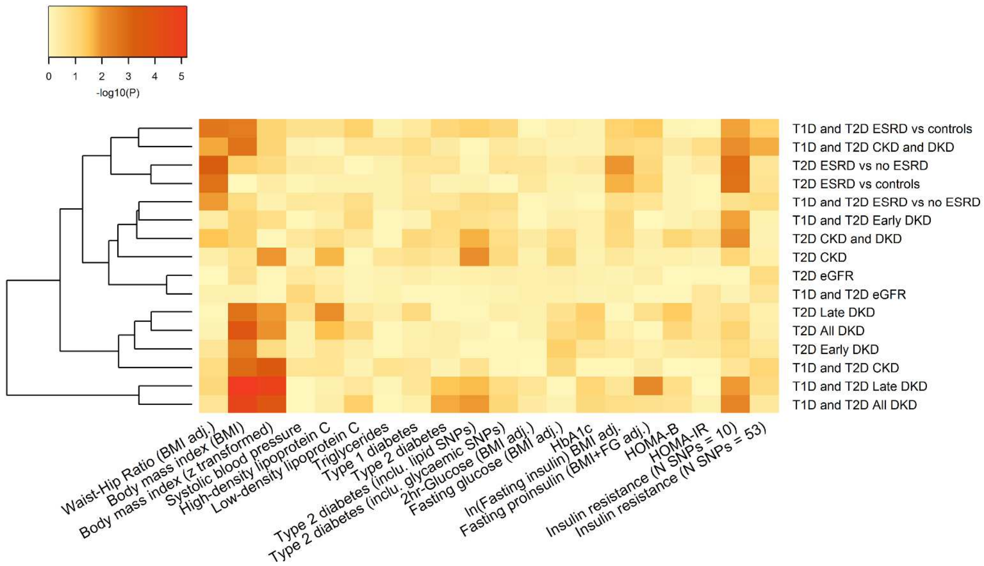

Figure 3: A heat map of genetic risk score associations with diabetic kidney disease (DKD) phenotypes in subjects with either type 1 diabetes or type 2 diabetes. A GRS for body mass index was significant after correction for multiple testing while other traits including systolic blood pressure were not associated with DKD phenotypes. Abbreviations used: chronic kidney disease (‘CKD’), end stage renal disease (‘ESRD’) and estimated glomerular filtration rate (‘eGFR’).

Online supplementary materials

S1 Table 1: Table of phenotypic characteristics

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S1 Table 2: Narrow sense ('chip') heritability of diabetic kidney disease phenotypes in subjects with type 2 diabetes estimated in the GoDARTS study

Phenotype*	Cases	Controls	h2	SE	pval
Chronic kidney disease	1,997	2,066	0.12	0.05	8.2×10^{-3}
All diabetic kidney disease	1,744	1,496	0.08	0.07	0.12
Estimated glomerular filtration rate	6,335		0.07	0.03	9.8×10^{-3}

*All cases are compared to subjects with type 2 diabetes and normoalbuminuria or an estimated glomerular filtration rate >60 mL/min/1.73m^2 unless otherwise stated.

S1 Table 3: Study characteristics for studies included in the discovery meta-analysis of the primary 'all diabetic kidney disease' phenotype

Diabetes	Cohort	Cases/controls	Age of onset of diabetes (cases/controls)	Age (cases/controls)	%Males (cases/controls)	BMI (cases/controls)	HbA1c (cases/controls)	Duration of diabetes (cases/controls)
2	SDR	1,250/580	54.5(12.6)/51.7(10.8)	65.5(11.7)/67.8(10.5)	65/52	30.2(5.3)/28.9(5.1)	7.2(1.2)/6.9(1.0)	10.9(8.70/16.1(6.0)
2	BENEDICT study phase A and B	188/165	53.4(8.6)/49.3(8.4)	66.3(11.0)/70.1(7.3)	177/58	2938(4.8)/27.8(4.1)	6.0(1.4)/5.8(1.4)	12.(9.5)/20.8(6.0)
2	STENO	163/131	46.1(9.2)/45.9(8.9)	61.2(7.5)/63.0(8.3)	60/62	29.8(5.2)/27.3(4.5)	9.1(1.7)/8.8(1.3)	15.3(7.1)/17.1(5.9)
2	GoDARTS 1*	885/816	68.6 (9.1)/66.2(8.8)	58.9(12.3)/54.0(12.1)	53/52	31.0(5.5)/31.0(5.4)	7.6(1.4)/7.5(1.3)	14.1(8.1)/16.5(6.8)
2	GoDARTS2*	859/680	67.9(11.6)/66.2(10.8)	72.1(11.2)/70.1(10.7)	60/60	31.5(6.1)/31.2(6.1)	7.5(1.5)/7.5(1.3)	11.4(6.9)/15.5(5.5)

*GoDARTS was typed on two genotyping arrays

S1 Table 4: Table of genotypic characteristics:

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S1 Table 5: Replication was sought for 164 variants and results were returned for 108 of these variants for six dichotomous phenotypes and estimated glomerular filtration rate (eGFR, mL/min/1.73m2) in subjects with type 2 diabetes.

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S1 Table 6: Rs9942471 was associated ($p \leq 5x10^{-8}$) with microalbuminuria in subjects with T2D of European descent and was not associated with any other dichotomous diabetic kidney disease phenotype.

Phenotype	CHR	BP	SNP	Discovery			Replication				Joint		
				EA/N EA EAF	OR (95%CI)	P	Ancestry	EAF	OR (95%CI)	P	OR (95%CI)	P	N
Chronic kidney disease (CKD)	6	89948232	rs9942471	A/C 0.63	0.98 (0.89,1.07)	0.50	European	0.62	1.10 (0.98,1.23)	0.10	1.02 (0.95,1.10)	0.41	11,897
							Asian and European	0.75	1.04 (0.96,1.13)	0.31	1.01 (0.95,1.08)	0.60	19,236
CKD and diabetic kidney disease (DKD)	6	89948232	rs9942471	A/C 0.63	1.06 (0.93,1.22)	0.32	European	0.59	1.20 (0.88,1.64)	0.45	1.07 (0.95,1.22)	0.22	2,834
							Asian and European	0.79	1.10 (0.88,1.37)	0.50	1.07 (0.95,1.21)	0.23	3,928
All DKD	6	89948232	rs9942471	A/C 0.64	1.20 (1.12,1.29)	$4.8x10^{-7}$	European	0.62	1.12 (0.98,1.27)	0.14	1.18 (1.11,1.25)	$3.8x10^{-7}$	7,053
							Asian and European	0.87	1.06 (0.98,1.15)	0.18	1.13 (1.07,1.19)	$1.7x10^{-4}$	19,253
End-stage renal disease (ESRD) vs non ESRD	6	89948232	rs9942471	A/C 0.64	0.85 (0.71,1.05)	0.07	European	0.63	1.09 (0.88,1.36)	0.42	0.94 (0.83,1.08)	0.30	6,455
							Asian and European	0.82	1.16 (1.00,1.36)	0.02	1.03 (0.93,1.13)	0.46	12,260
Late DKD	6	89948232	rs9942471	A/C 0.63	1.14 (1.04,1.25)	0.01	European	0.62	1.02 (0.86,1.20)	0.32	1.11 (1.02,1.20)	0.05	5,128
							Asian and European	0.88	1.01 (0.93,1.10)	0.85	1.06 (0.99,1.13)	0.22	19,578

				Discovery			Replication				Joint		
Phenotype	CHR	BP	SNP	EA/N EA EAF	OR (95%CI)	P	Ancestry	EAF	OR (95%CI)	P	OR (95%CI)	P	N
Microalbuminuria	6	89948232	rs9942471	A/C 0.64	1.24 (1.15,1.34)	2.1×10^{-7}	European	0.59	1.32 (1.09,1.59)	0.06	1.25 (1.16,1.34)	4.5×10^{-8}	4,801
							Asian and European	0.85	1.11 (0.99-1.23)	0.91	1.15 (1.08,1.23)	1.2×10^{-5}	5,652

S1Table 7: A cross comparison of top variants associated with diabetic kidney disease phenotypes in subjects with type 2 diabetes in subjects with type 1 diabetes (Shaded) (Sandholm et al, 2017).

Phenotype	SNP	EA/NEA	EAF	In subjects with type 2 diabetes		In subjects with type 1 diabetes	
				OR/Beta (95%CI)	*p*	OR/Beta (95%CI)	*p*
'CKD'	rs2206136 (*PLCB4*)	A/T	0.42	1.13 (1.05,1.21)	9.0×10^{-5}	0.94 (0.85,1.04)	0.23
'microalbuminuria'	rs9942471 (*GABRR1*)	A/C	0.64	1.25 (1.16,1.34)	4.50×10^{-8}	0.93 (0.82,1.05)	0.26
'eGFR'	rs11864909 (*UMOD*)	T/C	0.28	2.31 (1.54,3.09)	4.60×10^{-9}	1.22 (-0.06,2.50)	0.07
'ESRD vs no ESRD'	rs61277444 (*PTPN13*)	G/A	0.09	Not available		1.41 (1.21,1.65)	1.90×10^{-6}
'ESRD vs controls'	rs61277444 (*PTPN13*)	G/A	0.09			1.42 (1.02,1.67)	6.00×10^{-6}
'ESRD vs no ESRD'	rs7562121 (*AFF3*)	C/G	0.23	1.12 (0.97,1.30)	0.21	1.27 (1.17,1.39)	3.50×10^{-7}
'CKD+DKD'	rs1989248 (*CNTNAP2*)	C/A	0.28	0.73 (0.61,0.87)	6.14×10^{-4}	1.26 (1.15,1.38)	6.00×10^{-7}
'ESRD vs controls'	rs1989248 (*CNTNAP2*)	C/A	0.28	0.71 (0.57,0.88)	0.51	1.29 (1.17,1.43)	1.80×10^{-6}
'All DKD'	rs72809865 (*NRG3*)	T/C	0.16	1.11 (0.99,1.75)	0.05	1.17 (1.09,1.26)	7.40×10^{-6}

S1 Table 8: Phenotype definitions used in the combined analysis of diabetic kidney disease in subjects with type 1 diabetes or type 2 diabetes (T1D+T2D)

Analysis	Case definition	Control definition	Type 1 and 2 diabetes	
			#Cases	**#Controls**
All Diabetic kidney disease (DKD)	**All DKD**: Microalbuminuria OR OR Late DKD OR end-stage renal disease (ESRD)	Normoalbuminuria **(**Albumin excretion rate [AER] <20 µg/min OR AER <30 mg/24 h OR ACR <2.5/3.5 mg/mmol for men/women AND duration of T2D >10 years or duration of T1D >15 years	5,908	4,965
Microalbuminuria	**Microalbuminuria**: At least 2 out of 3 consecutive measurements with albumin excretion rate (AER) ≥20 AND <200 µg/min OR AER ≥30 AND <300 mg/24 hr OR albumin to creatinine ratio (ACR) ≥2.5/3.5 AND <25/35 mg/mmol for men/women	Normoalbuminuria AND duration of T2D >10 years or duration of T1D >15 years	2,795	4,831
Late DKD	**Late DKD**: At least one measurement with AER ≥200 µg/min OR AER ≥300 mg/24 h OR ACR ≥25/35 mg/mmol for men/women) or end-stage renal disease (ESRD, eGFR < 15 mL/min/1.73m^2 OR kidney transplantation OR dialysis)	Normoalbuminuria AND duration of T2D >10 years or duration of T1D >15 years	3,096	4,965
ESRD vs. controls	**ESRD**: eGFR < 15 mL/min/1.73m^2 OR kidney transplantation OR dialysis	No DKD AND duration of T2D >10 years or duration of T1D >15 years	1,184	4,474
ESRD vs. no ESRD	ESRD (see above)	No ESRD AND duration of T2D >10 years or duration of T1D >15 years	1,184	8,466
Chronic Kidney Disease (CKD)	**CKD**: eGFR < 60 mL/min/1.73m^2	No CKD AND duration of T2D >10 years or duration of T1D >15 years	5,554	3,680

Analysis	Case definition	Control definition	Type 1 and 2 diabetes	
			#Cases	#Controls
CKD and DKD	**CKD and DKD**: eGFR < 60 mL/min/1.73m^2 AND DKD	No CKD AND no ESRD AND normoalbuminuria AND duration of T2D >10 years or duration of T1D >15 years	2,647	2,995
eGFR	**eGFR**: eGFR=32788 x Serum Creatinine(µmol/L)$^{-1.154}$ x Agx10-$^{.203}$ x [0.742 if female] (mL/min/1.73m^2)		13,158	eGFR

S1 Table 9: The discovery, replication and joint analysis of the 47 lead variants selected for replication from seven dichotomous diabetic kidney disease and a continuous eGFR phenotype (mL/min/1.73m2) in the combined analysis of subjects with either type 1 or type 2 diabetes

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S1 Table 10: We report associations of reported diabetic kidney disease (DKD) variants with corresponding DKD phenotypes in this study at a p<0.05 irrespective of type of diabetes. In supplementary Figure 5 we show z scores for all DKD phenotypes from subjects with T2D and the combined analysis of subjects with T1D or T2D.

		Published						**Current study**			
PMID	**SNP (Gene)**	**Phenotype**	**Diabetes**	**EA**	**EAF**	**Effect (95%CI)**	**P**	**trait**	**Diabetes**	**Effect (95%CI)**	**P**
15793268	rs1800764 (*ACE*)	Microalbuminuria	T1D	C	0.46	1.11 (1.01,1.22)	0.04	'Microalbuminuria'	T2D	0.87 (0.78,0.97)	0.02
19430482	rs12917707 (*UMOD*)	CKD	-	G	0.80	1.32 (1.24,1.4)	5.2×10^{-16}	'CKD'	T1D+T2D	1.06 (0.99,1.14)	0.02
									T2D	1.08 (0.99,1.18)	0.02
									T1D+T2D	1.93 (1.25,2.61)	2.9×10^{-6}
	rs12917707 (*UMOD*)	eGFR	-	T	0.20	0.02 (0.02,0.03)	2.3×10^{-12}	'eGFR'	T1D+T2D	0.02 (0.01,0.03)	6.2×10^{-6}
									T2D	1.96 (1.20,2.73)	0.05
	rs17319721 (*SHROOM3*)	eGFR	-	A	0.44	0.01 (0.01,0.02)	1.0×10^{-12}	'eGFR'	T1D+T2D	-1.11 (-1.88,-0.34)	4.9×10^{-3}
	rs2467853 (*SPATAGL1*)	eGFR	-	G	0.39	0.01 (0.01,0.02)	6.0×10^{-14}	'eGFR'	T1D+T2D	-0.95 (-1.75,-0.149)	0.02
20383146	rs7805747 (*PRKGA2*)	CKD	-	A	0.24	1.18 (1.11,1.25)	4.0×10^{-12}	'CKD'	T1D+T2D	1.09 (1,1.18)	0.01
								'CKD'	T2D	1.10 (0.99,1.22)	0.03
20962522	rs1800783 (*NOS3*)	DKD	T1D	T	0.63	1.26 (1.1,1.45)	6.0×10^{-4}	'all DKD'	T1D+T2D	1.06 (0.99,1.13)	0.03
	rs5186 (*AGTR1*)	DKD	T1D+T2D	A	0.74	1.01 (0.93,1.10)	0.10	'all DKD'	T1D+T2D	0.90 (0.84,0.97)	5.8×10^{-3}
								'all DKD'	T2D	0.90	0.02

PMID	SNP (Gene)	Published						Current study			
		Phenotype	Diabetes	EA	EAF	Effect (95%CI)	P	trait	Diabetes	Effect (95%CI)	P
										(0.81,0.99)	
23028342	rs833061 (*VEGFA*)	DKD	T1D+T2D	T	0.5	2.08 (1.64,2.65)	0.32	'all DKD'	T2D	0.91 (0.84,0.98)	0.03
	rs12437854 (*RGMA/MCTP2*)	ESRD	T1D	G	0.06	1.72 (1.36,2.18)	2.0×10^{-9}	'ESRD vs controls'	T1D+T2D	1.30 (0.99,1.71)	3.6×10^{-3}
								ESRD vs non ESRD	T1D+T2D	1.40 (1.06,1.85)	1.2×10^{-3}
	rs7583877 (*AFF3*)	ESRD	T1D	C	0.31	1.34 (1.21,1.48)	1.2×10^{-8}	'ESRD vs controls'	T1D+T2D	1.21 (1.11,1.31)	1.9×10^{-3}
								'ESRD vs non ESRD'	T1D+T2D	1.22 (1.13,1.32)	4.8×10^{-4}
24871321	rs12137135 (*WNT4-ZBTB40*)	ESRD	T1D	G	0.16	Bayesian Analysis		'ESRD vs controls'	T1D+T2D	1.20 (1.02,1.40)	0.02
								'ESRD vs non ESRD'	T1D+T2D	1.23 (1.06,1.43)	8.1×10^{-3}
	rs12917114 (*SEMA6D-SLC24A5*)	ESRD	T1D	T	0.12			ESRD vs non ESRD	T1D+T2D	1.24 (1.05,1.46)	7.9×10^{-3}
	rs1670754 (4p15)	ESRD	T1D	A	0.19			'ESRD vs non ESRD'	T1D+T2D	1.16 (1.02,1.32)	0.04
	rs2838302 (*SIK1*)	ESRD	T1D	G	0.08			'ESRD vs controls'	T1D+T2D	1.28 (1.03,1.58)	4.7×10^{-3}
								'ESRD vs non ESRD'	T1D+T2D	1.39 (1.12,1.74)	3.9×10^{-4}

S1 Table 11: Results of a genetic risk score analysis of diabetic kidney disease (DKD) related risk factors and different DKD phenotypes ($p<2.3x10^{-3}$)

DKD PHENOTYPE	GENETIC RISK SCORE	OR(95%CI)	PVAL
T1D and T2D Late DKD	Body mass index (BMI)	2.12 (1.55,2.90)	2.3×10^{-6}
T1D and T2D Late DKD	Body mass index (z transformed)	2.04 (1.48,2.82)	1.6×10^{-5}
T1D and T2D All DKD	Body mass index (BMI)	1.75 (1.35,2.27)	2.4×10^{-5}
T1D and T2D All DKD	Body mass index (z transformed)	1.68 (1.28,2.19)	1.5×10^{-4}
T2D All DKD	Body mass index (BMI)	2.02 (1.40,2.92)	1.8×10^{-4}
T1D and T2D CKD	Body mass index (z transformed)	1.73 (1.29,2.32)	2.7×10^{-4}
T2D ESRD vs no ESRD	Waist-Hip Ratio (BMI adj.)	4.19 (1.87,9.36)	4.8×10^{-4}
T1D and T2D CKD	Body mass index (BMI)	1.62 (1.21,2.17)	1.3×10^{-3}
T2D ESRD vs no ESRD	Insulin resistance (N SNPs = 10)	1.09 (1.03,1.14)	1.6×10^{-3}
T2D ESRD vs controls	Insulin resistance (N SNPs = 10)	1.09 (1.03,1.15)	1.7×10^{-3}
T2D ESRD vs controls	Waist-Hip Ratio (BMI adj.)	4.04 (1.69,9.66)	1.7×10^{-3}
T2D Late DKD	Body mass index (BMI)	2.12 (1.32,3.40)	1.8×10^{-3}
T1D and T2D CKD and DKD	Body mass index (BMI)	1.84 (1.25,2.70)	1.8×10^{-3}

S1 Table 12: The Finnish Diabetic Nephropathy Study Centres

Centre	Members
Anjalankoski Health Center	S.Koivula, T.Uggeldahl
Central Finland Central Hospital, Jyväskylä	T.Forslund, A.Halonen, A.Koistinen, P.Koskiaho, M.Laukkanen, J.Saltevo, M.Tiihonen
Central Hospital of Åland Islands, Mariehamn	M.Forsen, H.Granlund, A.-C.Jonsson, B.Nyroos
Central Hospital of Kanta-Häme, Hämeenlinna	P.Kinnunen, A.Orvola, T.Salonen, A.Vähänen
Central Hospital of Kymenlaakso, Kotka	R.Paldanius, M.Riihelä, L.Ryysy
Central Hospital of Länsi-Pohja, Kemi	H.Laukkanen, P.Nyländen, A.Sademies
Central Ostrobothnian Hospital District,Kokkola	S.Anderson, B.Asplund, U.Byskata, P.Liedes,M.Kuusela, T.Virkkala
City of Espoo Health Center	
Espoonlahti	A.Nikkola, E.Ritola
Tapiola	M.Niska, H.Saarinen
Samaria	E.Oukko-Ruponen, T.Virtanen
City of Helsinki Health Center	Viherlaakso A.Lyytinen
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Suutarila	A.Kaprio, J.Kärkkäinen, B.Rantaeskola
Töölö	P.Kääriäinen, J.Haaga, A-L.Pietiläinen
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Martinlaakso	M.Laine, T.Pellonpää, R.Puranen
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Tikkurila	R.Lönnblad, A.Malm, J.Mäkelä, E.Rautamo
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Hospital of Lounais-Häme, Forssa	T.Kalliomäki, J.Koskelainen, R.Nikkanen, N.Savolainen, H.Sulonen, E.Valtonen
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Iisalmi Hospital	E.Toivanen
Jokilaakso Hospital, Jämsä	A.Parta, I.Pirttiniemi
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Central Hospital of Åland Islands, Mariehamn	M.Forsen, H.Granlund, A.-C.Jonsson, B.Nyroos
Central Hospital of Kanta-Häme, Hämeenlinna	P.Kinnunen, A.Orvola, T.Salonen, A.Vähänen
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Tapiola	M.Niska, H.Saarinen
Samaria	E.Oukko-Ruponen, T.Virtanen
City of Helsinki Health Center	Viherlaakso A.Lyytinen
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S1 Table 13: Hong Kong Diabetes Registry TRS Project Group members.

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S1 Table 14: Group membership of The Warren 3/UK GoKinD Study Group

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S1 Table 16: DCCT/EDIC group members

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02	University of Pennsylvania	Patti Bourne	Mark Schutta
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05	Joslin Diabetes Center	Ellen Golden	Lloyd Aiello
06	Massachusetts General Hospital	Mary Larkin	David Nathan
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09	International Diabetes Center	Mary Johnson Kimberly Gunyou	Richard Bergenstal
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11	University of Minnesota	Nancy Flaherty	John Bantle
12	University of Missouri	Susan Hitt	David Goldstein Dean Hainsworth
13	University of Pittsburgh	Lori Cimino	Trevor Orchard
14	University of Tennessee	Christine Wigley	Samuel Dagogo-Jack
15	University of Texas	Suzanne Strowig	Philip Raskin
16	University of Toronto	Annette Barnie	Bernard Zinman
17	University of Washington	Robyn Fahlstrom	Jerry Palmer
18	University of Western Ontario	Judith Harth Marsha Driscoll	Charlotte McDonald
19	Vanderbilt University	Janie Lipps Hagan	Michael May
20	Washington University St. Louis	Lucy Levandoski	Neil White

CLINIC #	CLINIC NAME	STUDY	PRINCIPAL
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25	University of MD Baltimore	Sherry Johnsonbaugh	Ryan Miller
26	University of New Mexico	Janene Canady	David Schade
27	University of South Florida	Maria Luisa Bernal	John Malone Anthony Morrison
41	University of Michigan	Catherine Martin	William Herman Rodica Pop-Busui

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	NIDDK Project Scientist	Catherine Cowie
	NIDDK Program Director	Ellen Leschek
	Lead Research Scientist	Patricia Cleary
	Principal Investigator Data Coordinating Center	John Lachin
	Vice Chairman Chair, P&P Committee	Bernie Zinman
	Principal Investigator Clinical Coordinating Center	Rose Gubitosi-Klug
	Co-Chair, Study Coordinators Chair, DQA Committee	Gayle Lorenzi
	Co-Chair, Study Coordinators	Catherine Martin
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	Project Manager	Valerie Arends
	Director	Barbara Blodi
	Principal Investigator	Ronald Danis
	Project Manager	Daniel Lawrence
	Lead Photographer	Hugh Wabers
	Director	Elsayed Soliman
	Senior MD Coder	Zhu-Ming Zhang
	Programmer/Analyst	Charles Campbell
	Senior ECG Technician	Susan Hensley
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S1 Table 17: Members of the SUMMIT consortium

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	Alexander Ehlgen	Transmed
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	Jochen Huber	In vivo Scientist CMDR, Head of Lab
	Corinna Schölch	Biomarker & Bioanlysis, Head of Lab
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2	**Leif Groop**	Prof. Endocrinology; Coordinator Managing entity IMI-JU; PI; **WP1 and WP6 leader**
Lund University	Elisabet Agardh	Prof. Ophthalmology
Clinical Research Centre	Emma Ahlqvist	Postdoc
Malmö, Sweden	Tord Ajanki	Communication strategist
	Nibal Al Maghrabi	Research nurse
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	Jan Apelqvist	Diabetologist
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	Malin Neptin	Biomedical analyst
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	Gerd Östling	Laboratory Engineer
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	Päivi Tikka-Kleemola	Service manager
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	Maria Nastase-Mannila	Postdoc
	Jaako Patrakka	Postdoc
	Angela Silveira	Assoc. Prof. Cardiovascular genetics
	Rona Strawbridge	Postdoc
	Karl Tryggvason	Prof. Medical Chemistry
	Max Vikström	Statistician
	John Öhrvik	Professor
	Anne-May Österholm	Postdoc
5	**Barbara Thorand**	Nutritional scientist, epidemiologist
Helmholtz Centre	Christian Gieger	Statistician
Munich, Germany	Harald Grallert	Biologist
	Tonia Ludwig	Statistician
	Barbara Nitz	Scientist
	Andrea Schneider	Data manager
	Rui Wang-Sattler	Scientist
	Astrid Zierer	Statistician
6	**Giuseppe Remuzzi**	Institute director; PI
Mario Negri Institute for	Ariela Benigni	Head of department Molecular Medicine
Pharmacological Research	Roberta Donadelli	Scientist
	Maria Domenica Lesti	Researcher
Bergamo, Italy	Marina Noris	Head Laboratory Immunology and genetics of transplantation and rare diseases
	Norberto Perico	Senior scientist
	Annalisa Perna	Biostatistician
	Rossella Piras	Postdoc
	Piero Ruggenenti	Head of department Renal medicine, Assist. Prof. Nephrology and dialysis
	Erica Rurali	Postdoc
7	**David Dunger (att: Jane Horsford)**	Prof. Paediatrics; PI
University of Cambridge	Ludo Chassin	Senior Data Manager
UK	Neil Dalton, London	Clinical biochemistry
	John Deanfield, London	Paediatric cardiology
	Jane Horsford	PA to Prof. Dunger
	Clare Rice	Operations manager/financial contact
	James Rudd	Cardiovascular imaging
	Neil Walker	Head Data services

Partner	Name	Position
	Karen Whitehead	Technician
	Max Wong	Postdoc
8	**Helen Colhoun**	Prof. Public health and epidemiology; PI; Vice coordinator Managing entity; **WP2 leader**
	Fiona Adams	
University of Dundee	Tahira Akbar	PA to Helen Colhoun
Scotland	Jill Belch	Prof. Vasucular disease
	Harshal Deshmukh	PhD student
	Fiona Dove	
	Angela Ellingford	NHS Tayside Diabetic Retinopathy Screening Programme manager
	Bassam Farran	Statistician
	Mike Ferguson	Dean of research Biological chemistry and drug discovery
	Gary Henderson	
	Graeme Houston	Consultant radiologist/senior lecturer
	Faisel Khan	Reader, Vascular & Inflammatory Diseases Research Unit
	Graham Leese	Consultant diabetologist/reader
	Yiyuan Liu	PhD student
	Shona Livingstone	Senior statistician
	Helen Looker	Epidemiologist
	Margaret McCann	Project assistant
	Stuart McGurnaghan	Lead data programmer
	Andrew Morris	Prof. Diabetic medicine
	David Newton	
	Colin Palmer	Prof. Pharmacogenomics
	Ewan Pearson	Consultant diabetologist/senior lecturer
	Gillian Reekie	Research Nurse
	Natalie Smith	Research Nurse
9	**Angela Shore**	Prof. Cardiovascular Science, PI
Peninsula Medical School	Kuni Aizawa	Postdoc
Exeter, UK	Claire Ball	Research nurse
	Nick Bellenger	Cardiologist
	Francesco Casanova	Associate Research Fellow Vascular medicine
	Tim Frayling	Prof. Genetics
	Phil Gates	Senior lecturer Cardiovascular science
	Kim Gooding	Postdoc Vascular medicine
	Andrew Hatttersley	Prof. Molecular medicine
	Roland Ling	Consultant opthalmologist
	David Mawson	Research technician

Partner	Name	Position
	Robin Shandas	Prof. Bioengineering (Colorado)
	David Strain	Stroke physician, clinical lecturer
	Clare Thorn	Postdoc Vascular medicine
10	**Ulf Smith**	Prof. ; PI
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	Oluf Pedersen	Prof. Steno Centre, Copenhagen
	Georgio Sesti	Prof. Universtiy of Catanzaro
11	**Per-Henrik Groop**	Prof. Diabetes genetics; PI
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Folkhälsan	Carol Forsblom	Clinical coordinator
Helsinki, Finland	Valma Harjutsalo	
	Maikki Parkkonen	Laboratory manager
	Niina Sandholm	DSc(PhD); GWAS and bioinformatics
	Nina Tolonen	MD PhD
	Iiro Toppila	BSc, bioinformatician
	Erkka Valo	MSc, bioinformatician
12	**Veikko Salomaa**	Prof. Epidemiology; PI; **deputy leader WP2**
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Helsinki, Finland	Kati Kristiansson	Postdoc
	Pia Okamo	THL press officer
	Tomi Peltola	
	Markus Perola	Professor
	Arto Pietilä	Statistician
	Samuli Ripatti	Professor, Statistics
	Marketta Taimi	Research assistant
13	**Seppo Ylä-Herttuala**	Prof.; PI; **WP4 leader**
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Kuopio, Finland	Marike Dijkstra	PhD student
	Erika Gurzeler	PhD student
	Jenni Huusko	PhD student
	Ivana Kholová	Postdoc
	Markku Laakso	Prof.
	Mari Merentie	PhD student
	Marja Poikolainen	PA Prof Ylä-Herttuala

Partner	Name	Position
14	**Mark McCarthy**	Prof. Human type 2 diabetes; Oxford Centre for Diabetes, Endocrinology and Metabolism; Wellcome Trust Centre for Human Genetics; PI; **deputy leader WP1**
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	Fredrik Karpe	PI OCDEM
	Vasiliki Lagou	Postdoc
	Andrew Morris	Wellcome Trust Senior Fellow; Bioinformatics and statistical genetics
	Will Rayner	Database manager
	Neil Robertson	Informatics
	Natalie van Zuydam	Postdoc
15	**Claudio Cobelli**	Prof. ; PI; **WP5 leader**
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Italy	Francesca Finotello	PhD student
-	Francesco Sambo	Postdoctoral fellow
-	Gianna Toffolo	Prof.
-	Emanuele Trifoglio	PhD student
-	-	-
16	**Riccardo Bellazzi**	Prof. Bioengineering; PI; **deputy leader WP5**
	Nicola Barbarini	Postdoctoral fellow
University of Pavia	Mauro Bucalo	Software engineer
Italy	Christiana Larizza	Assist. Prof.
	Paolo Magni	Assoc. Prof.
	Alberto Malovini	Postdoctoral fellow
	Simone Marini	Postdoctoral fellow
	Francesca Mulas	Postdoctoral fellow
	Silvana Quaglini	Prof.
	Lucia Sacchi	Assist. Prof.
	Francesca Vitali	
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	Carmela Morizzo	Biologist, Sonographer Cardiovascular ultrasound
	Lucrecia Mota	EGIR administrative office
	Andrea Natali	Assoc. Prof. Medicine
	Carlo Palombo	Assoc. Prof. Medicine; **deputy leader WP3**
	Elena Venturi	Researcher

Partner	Name	Position
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18	**Carlo Patrono**	Prof.Pharmacology; PI
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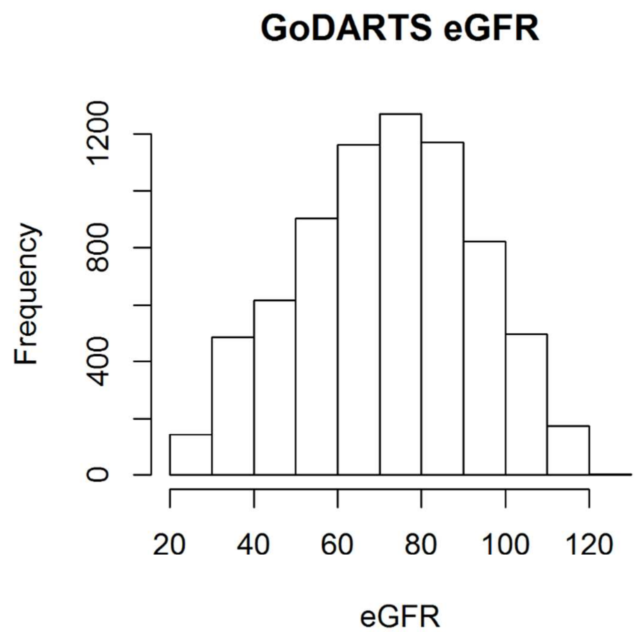
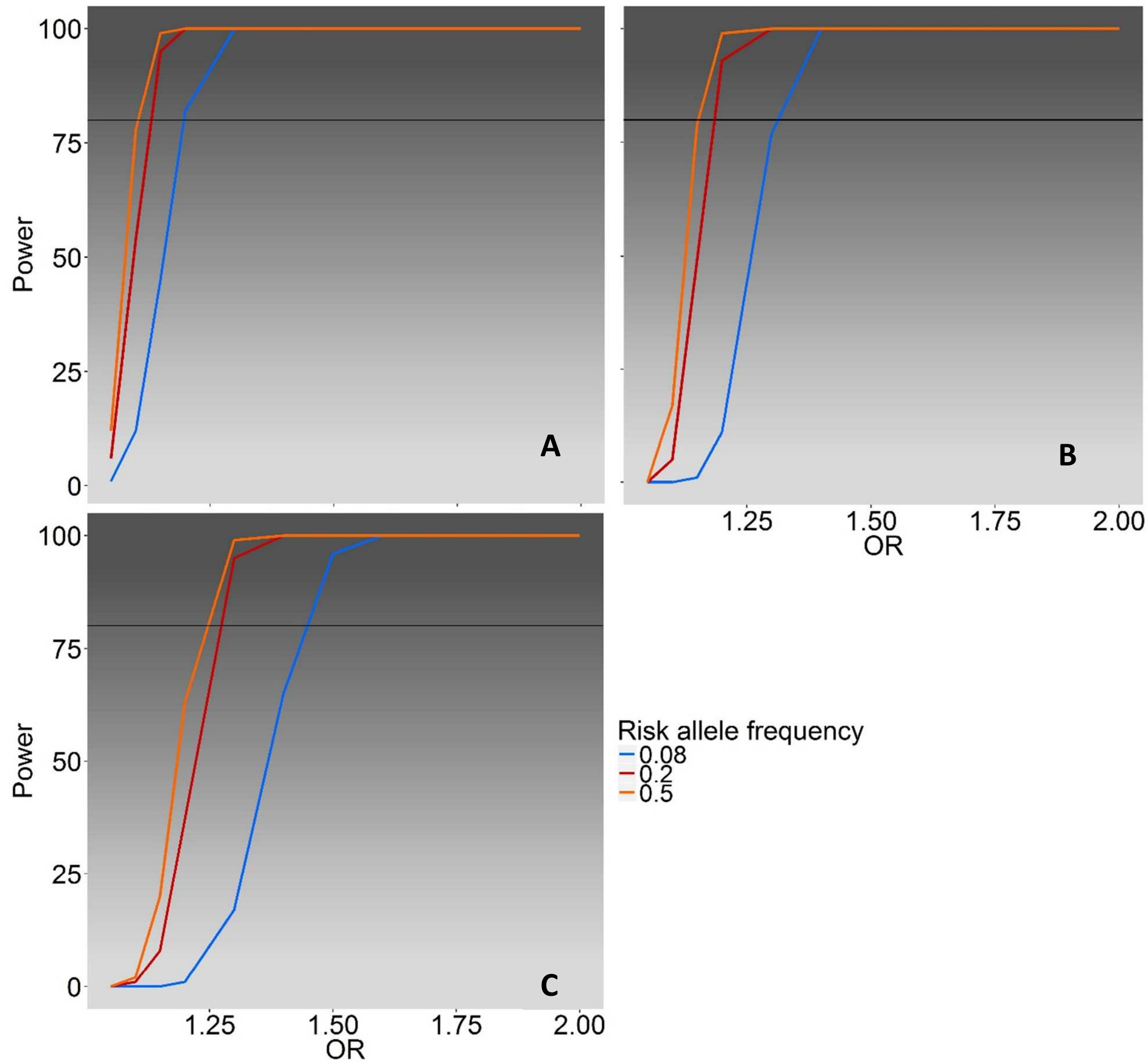
Italy	Bianca Rocca	Assist. Prof. Pharmacology
19	**Pirjo Nuutila**	Prof. ; PI
University of Turku	Johanna Haukkala	PhD student
Finland	Juhani Knuuti	Prof. ; Director Turku PET Centre
	Anne Roivainen	Prof.
	Antti Saraste	Adj. Prof.
20	**Paul McKeague**	Prof. Genetic Epidemiology; PI
University of Edinburgh	Norma Brown	Research administrator, Public Health Services
Scotland	Marco Colombo	Bioinformaticist
21	**Birgit Steckel-Hamann**	Deputy coordinator; PI, Manager IMI, LRL
Eli Lilly	Krister Bokvist	Biostatistician
	Sudha Shankar	Diabetologist
	Melissa Thomas	Translational Science
22	**Li-ming Gan**	Prof.; Translational Science Director Cardiovascular Disease; PI, **WP3 leader**
AstraZeneca	Suvi Heinonen	PhD, Internal AZ postdoc, Bioscience
	Ann-Cathrine Jönsson-Rylander	PhD, Assoc. Prof., Team Leader Bioscience, **WP4 leader**
	Remi Momo	Postdoctoral fellow
	Volker Schnecke	Informatician Translational Science, **WP5 leader**
	Robert Unwin	Translational Science Director Diabetic Nephropathy
	Anna Walentinsson	Geneticist Translational Science
	Carl Whatling	Bioscientist
23	**Everson Nogoceke**	Pre-clinical and clinical aspects of metabolic and vascular disease; PI; **WP2 leader**
Roche	Gonzalo Durán Pacheco	Senior Research Statistician
	Ivan Formentini	Biomarker & Experimental Medicine Leader
	Thomas Schindler	Pre-clinical and clinical and clinical biomarkers
24	**Piero Tortoli**	Professor of Electronics
University of Florence	Luca Bassi	Postdoctoral fellow

Partner	Name	Position
	Enrico Boni	Postdoctoral fellow
	Alessandro Dallai	Postdoctoral fellow
	Francesco Guidi	Technician
	Matteo Lenge	PhD student
	Riccardo Matera	PhD student
	Alessandro Ramalli	PhD student
	Stefano Ricci	Assist. Prof.
	Jacopo Viti	PhD student
25	**Bernd Jablonka**	SAD internal IMI coordinator
Sanofi-aventis	Dan Crowther	Biomarker researcher
	Johan Gassenhuber	Biostatistician
	Sibylle Hess	Biomarker researcher
	Thomas Hübschle	Pharmacologist Diabetes
	Hans-Paul Juretschke	Imaging
	Hartmut Rütten	Head Translational Medicine
	Thorsten Sadowski	Pharmacologist Diabetes
	Paulus Wohlfart	Pharmacologist Diabetes
26	**Julia Brosnan**	Biochemist, (pre)clinical research CVD, Pfizer US; **WP2 leader**
Pfizer	Valerie Clerin	Cardio-renal biologist, WP2
	Eric Fauman	Computational biologist
	Craig Hyde	Statistician
	Anders Malarstig	Human genetics, Pfizer Europé; **WP1 leader**
	Nick Pullen	Renal Disease Research Director
	Mera Tilley	
	Theresa Tuthill	Imaging specialist
	Ciara Vangjeli	Cardiovascular genetic epidemiologist, Pfizer Europe
	Daniel Ziemek	Computational biologist

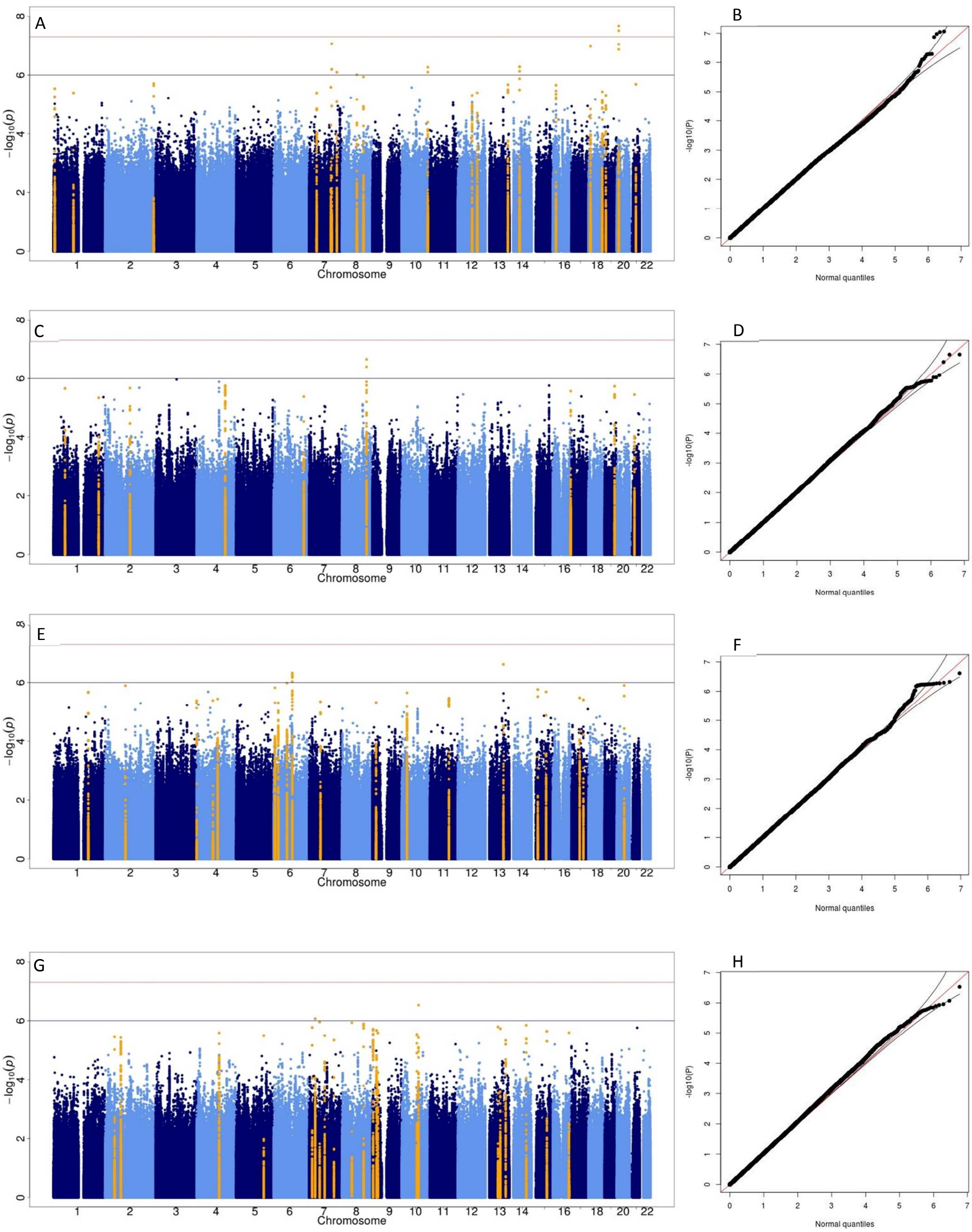
Figures

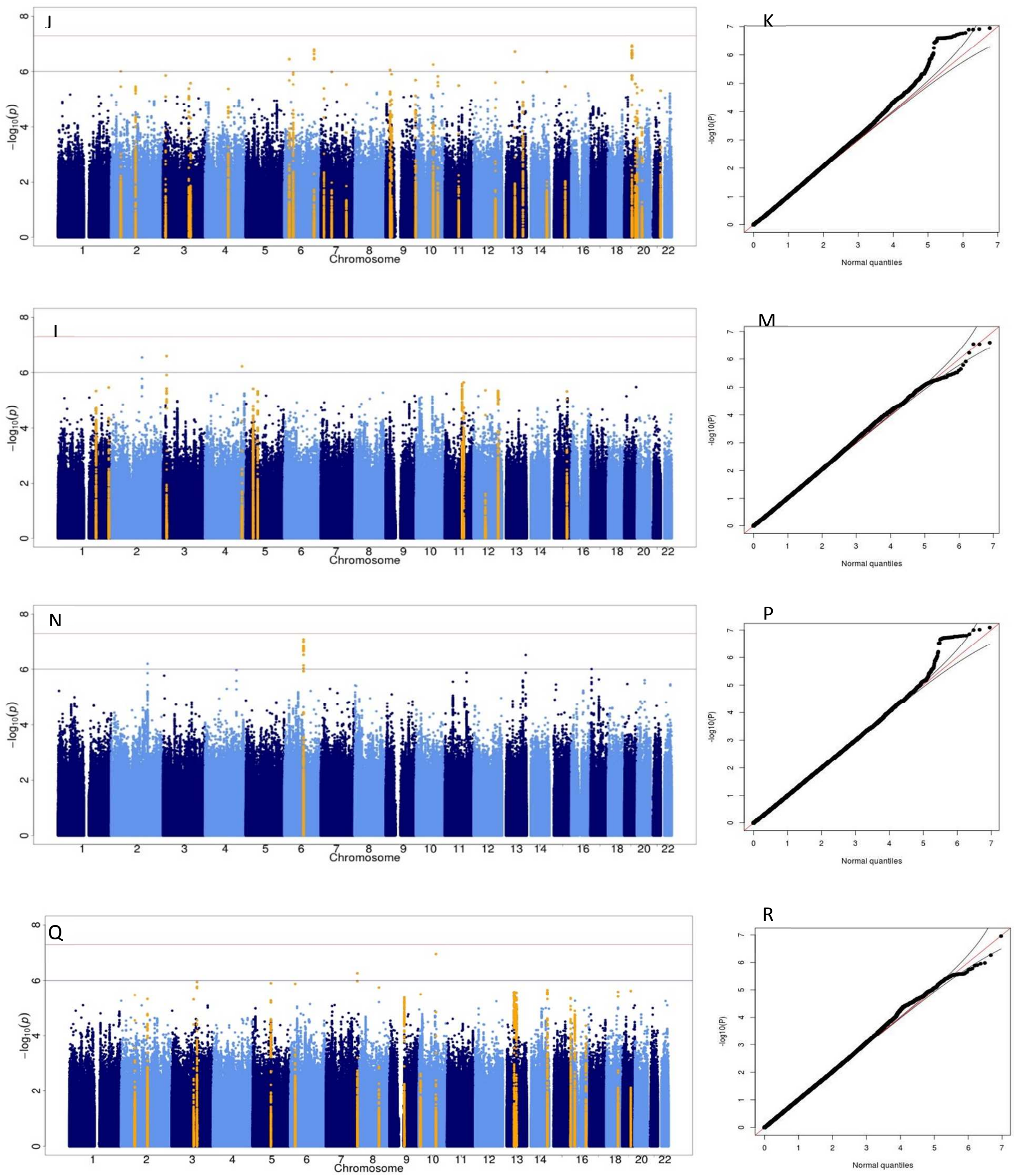


S1 Figure 1: Histogram of estimated glomerular filtration rate in the Genetics of Diabetes and Audit Research in Tayside Scotland study (N=6,335) shows an approximately normal distribution.

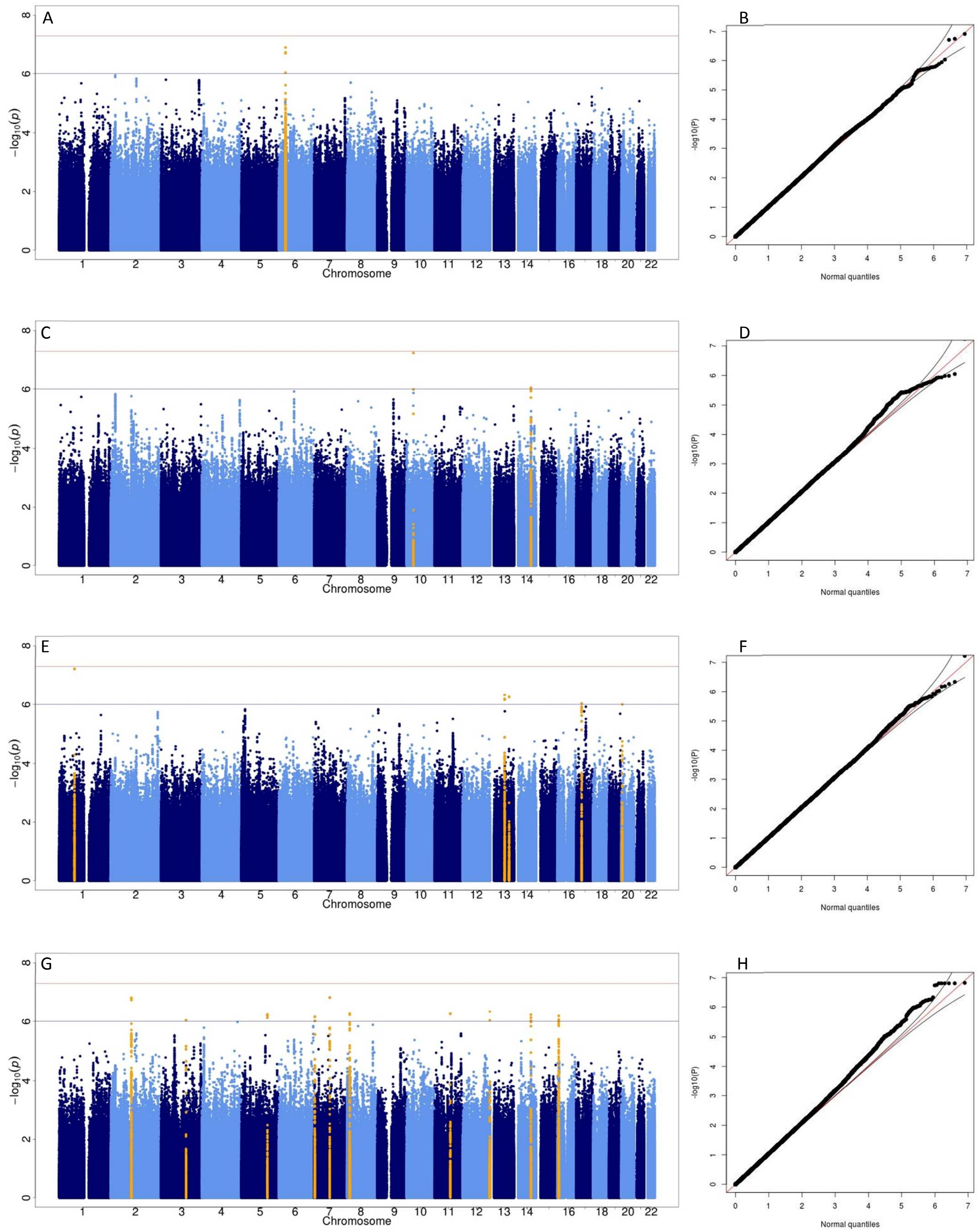


S1 Figure 2: Power calculations were performed for a range of OR (1.05-2.00) and a range of minor allele frequencies (0.08-0.50) in A: 5,908 diabetic kidney disease cases (DKD) and 4,965 controls with no history of DKD with either T2D or T1D to detect an association with a candidate gene $\alpha = 0.05/55 = 9x10^{-4}$); B: 5,908 DKD and 4,965 controls with no history of DKD with either T2D or T1D to detect an association at $\alpha = 5x10^{-8}$ and C: 3,345 DKD cases and 2,372 controls with no history of DKD in subjects with T2D to detect associations at $\alpha = 5x10^{-8}$.


A
B
C
D
E
F
G
H
$-\log_{10}(p)$
Chromosome
-log10(P)
Normal quantiles



S1 Figure 3: Manhattan and QQ plots of discovery p values for chronic kidney disease(CKD, plots A and B), CKD and diabetic kidney disease (DKD, plots C and D), ‘all DKD’ (plots E and F), end-stage renal disease compared to normoalbuminuric controls (ESRD, plots G and H), ESRD compared to normoalbuminuric controls and all other forms of DKD (plots J and K), ‘late DKD’ (plots L and M), microalbuminuria (plots N and P) and estimated glomerular filtration rate (plots Q and R) from the analysis of subjects with type 2 diabetes. Orange peaks represent signals selected for replication.


A
B
C
D
E
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G
H
$-\log_{10}(p)$
Chromosome
1
2
3
4
5
6
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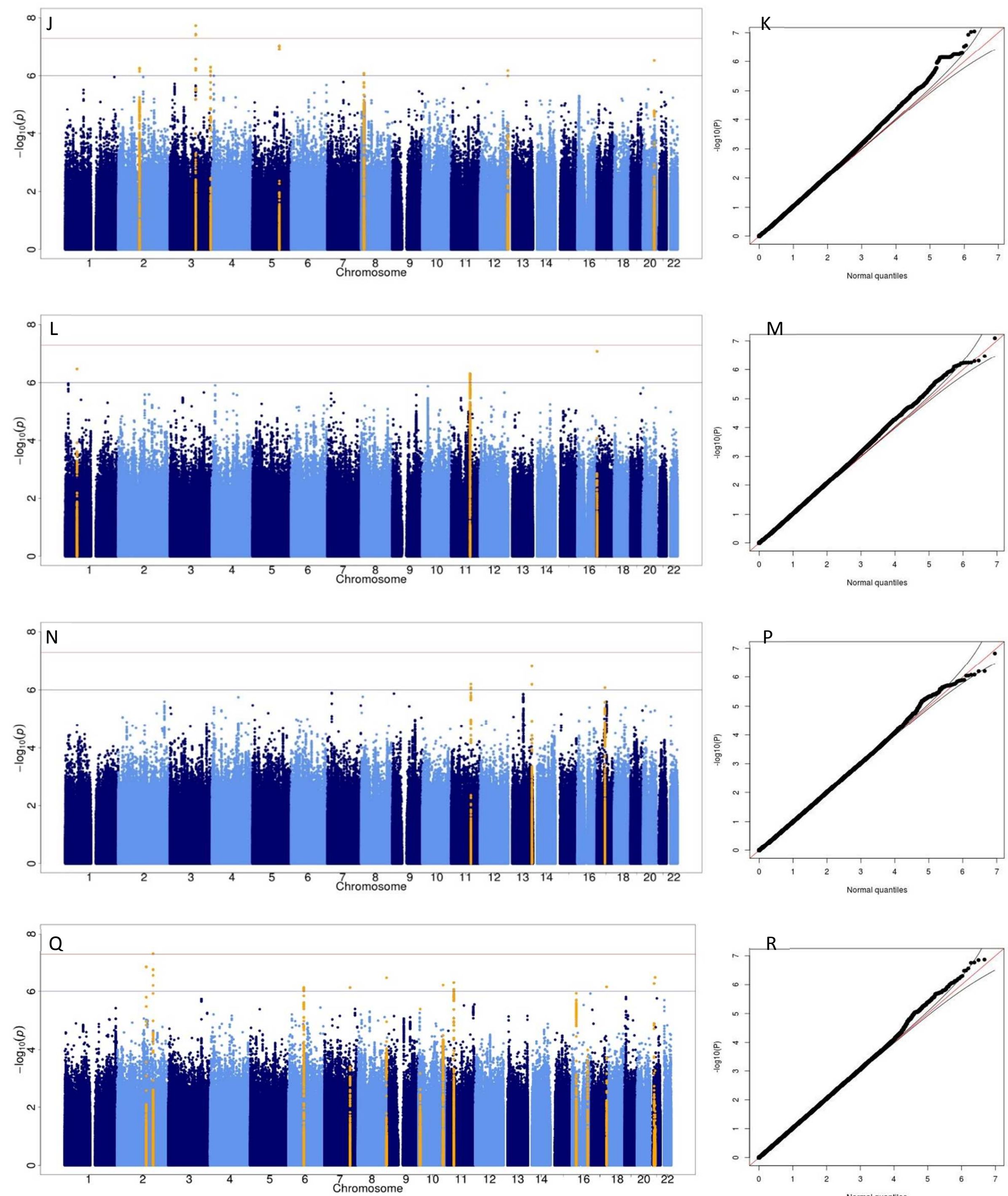
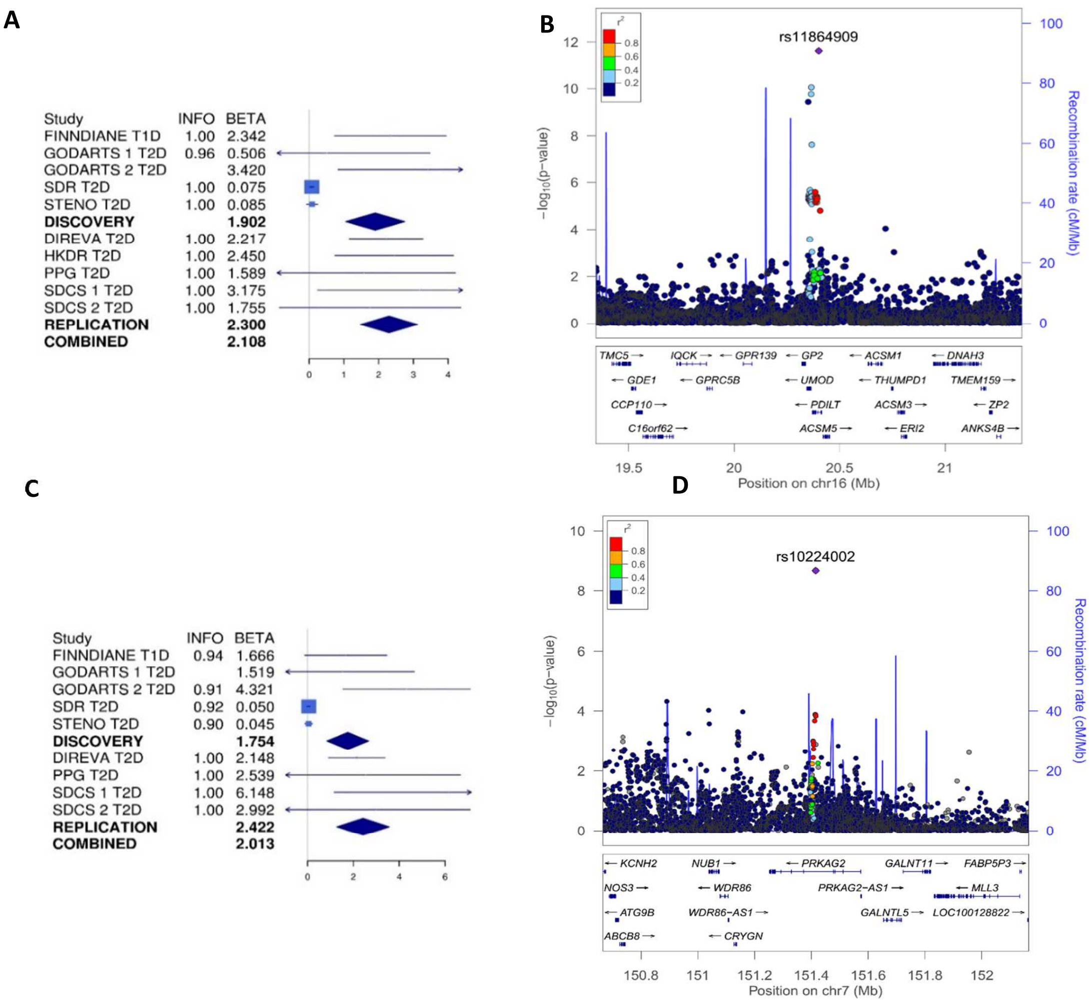
8
9
10
11
12
13
14
16
18
20
22
-log10(P)
Normal quantiles



S1 Figure 4: Manhattan and QQ plots for chronic kidney disease (CKD, plots A and B), CKD and diabetic kidney disease (DKD, plots C and D), 'all DKD' (plots E and F), end-stage renal disease compared to normoalbuminuric controls (ESRD, plots G and H), ESRD compared to normoalbuminuric controls and all other forms of DKD (plots J and K), 'late DKD' (plots L and M), microalbuminuria (plots N and P) and estimated glomerular filtration rate (plots Q and R) from the combined analysis of subjects with type 1 diabetes and type 2 diabetes. Orange peaks represent signals selected for replication.



S1 Figure 5: Two genome-wide significant ($p<5x10^{-8}$) loci for eGFR from the combined analysis of subjects with either type 1 or type 2 diabetes. These loci map to two signals in *UMOD* and *PRKAG2* respectively (A and B). The Locuszoom plots show the locus specific association signal and the forest plots (C and D) the individual study effects or the top SNP.

S1 Figure 6: Sixty-one loci have been reported for diabetic kidney disease (DKD) in the literature. In this study we had summary statistics for 55 of these loci. The lattice plot shows the z score for the reported loci aligned to the risk or trait raising allele of the original report. The plot also reflects whether the original report was from subjects with diabetes (T1D+T2D,T1D or T2D) or irrespective of diabetes status (type of diabetes not indicated).

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Data availability

The summary level GWAS is available at www.imi-summit.eu. Raw genotypic and phenotypic data will be made available for researchers who meet the criteria for access to confidential data for the following data: SDR: at www.imi-summit.eu; NFS-ORPS through JDRF/WT Diabetes and Inflammation Laboratory (DIL) in Cambridge (https://www-gene.cimr.cam.ac.uk/). The written consents of the FinnDiane, Eurodiab, GoDARTS and Steno studies do not allow sharing individual-level genotype or phenotype data (The authors of these studies may be contacted for collaboration: Per-Henrik Groop, per-henrik.groop@helsinki.fi; Helen Colhoun, H.Colhoun@dundee.ac.uk, Peter Rossing, pro@steno.dk, respectively).

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